GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:01:39 ; Search time 50.6667 Seconds
(without alignments)
3886.887 Million cell updates/sec

Title: US-09-806-194A-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3651	100.0	697	3	AAY88428	Aay88428 Human APP
2	3651	100.0	697	4	AAU07208	Aau07208 Human bet
3	3651	100.0	697	4	AAE10635	Aae10635 Human amy
4	3651	100.0	697	4	AAE06865	Aae06865 Human amy
5	3651	100.0	697	4	AAE02587	Aae02587 Human amy
6	3651	100.0	697	4	AAU06609	Aau06609 Human Amy
7	3651	100.0	697	5	ABB78596	Abb78596 Human APP
8	3646	99.9	697	3	AAY88430	Aay88430 Human APP
9	3646	99.9	697	4	AAU07210	Aau07210 Human bet

10	3646	99.9	697	4	AAE10637	Aae10637 Human amy
11	3646	99.9	697	4	AAE06867	Aae06867 Human amy
12	3646	99.9	697	4	AAE02589	Aae02589 Human amy
13	3646	99.9	697	4	AAU06611	Aau06611 Human Amy
14	3646	99.9	697	5	ABB78598	Abb78598 Human APP
15	3646	99.9	740	7	ADB87314	Adb87314 Human amy
16	3646	99.9	740	7	ADB87312	Adb87312 Human amy
17	3643	99.8	697	3	AAY88429	Aay88429 Human APP
18	3643	99.8	697	4	AAU07209	Aau07209 Human bet
19	3643	99.8	697	4	AAE10636	Aae10636 Human amy
20	3643	99.8	697	4	AAE06866	Aae06866 Human amy
21	3643	99.8	697	4	AAE02588	Aae02588 Human amy
22	3643	99.8	697	4	AAU06610	Aau06610 Human Amy
23	3643	99.8	697	5	ABB78597	Abb78597 Human APP
24	3641	99.7	695	1	AAP81692	Aap81692 Sequence
25	3641	99.7	695	2	AAR26338	Aar26338 APP695. 3
26	3641	99.7	695	2	AAY20233	Aay20233 Human bet
27	3641	99.7	695	2	AAY07221	Aay07221 Amyloid p
28	3641	99.7	695	3	AAY88434	Aay88434 Human APP
29	3641	99.7	695	3	AAY44705	Aay44705 Human bet
30	3641	99.7	695	4	AAE10632	Aae10632 Human wil
31	3641	99.7	695	4	AAE06862	Aae06862 Human wil
32	3641	99.7	695	4	AAE02584	Aae02584 Human amy
33	3641	99.7	695	4	AAU06606	Aau06606 Human Amy
34	3641	99.7	695	5	ABB78593	Abb78593 Human APP
35	3641	99.7	695	5	AAG68315	Aag68315 Human amy
36	3641	99.7	695	5	ABG32721	Abg32721 Human amy
37	3641	99.7	695	6	ABP97918	Abp97918 Amino aci
38	3641	99.7	695	6	ABB99604	Abb99604 Amino aci
39	3641	99.7	695	7	ADB87311	Adb87311 Human amy
40	3641	99.7	695	7	ADB33519	Adb33519 Human APP
41	3641	99.7	695	7	ADC65997	Adc65997 Human APP
42	3638	99.6	695	2	AAY49690	Aay49690 Human bet
43	3636	99.6	695	2	AAW19481	Aaw19481 APP695 mu
44	3636	99.6	695	2	AAW19484	Aaw19484 APP695 mu
45	3636	99.6	695	2	AAW19498	Aaw19498 APP695 mu

ALIGNMENTS

RESULT 1
AAY88428
ID AAY88428 standard; protein; 697 AA.
XX
AC AAY88428;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP696-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP696-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.

XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15665.
XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Claim 132; Page 137-141; 183pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 2
AAU07208
ID   AAU07208 standard; protein; 697 AA.
XX
AC   AAU07208;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-KK.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-KK.
XX
OS   Homo sapiens.
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
```

PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR N-PSDB; AAS11708.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 6; Page 144-146; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of human amyloid
CC protein precursor, APP695-KK, used in the method of the invention
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 3
AAE10635
ID AAE10635 standard; protein; 697 AA.
XX
AC AAE10635;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX
KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP695-KK;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
XX
OS Homo sapiens.

OS Synthetic.
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17871.
XX
PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Example 6; Page 114-116; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic acti0ity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-KK (APP695-KK) isoform which is obtained by the
CC addition of two Lys residues (KK motif) at the C-terminus of APP695
CC protein
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 4
AAE06865
ID   AAE06865 standard; protein; 697 AA.
XX
AC   AAE06865;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;
KW   mutein.
```

XX
OS Homo sapiens.
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
DR N-PSDB; AAD13027.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 6; Page 144-146; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is modified human amyloid precursor protein 695-KK
CC (APP695-KK) isoform. APP695-KK isoform is obtained by addition of two Lys
CC residues (KK motif) at the C-terminal end of APP695 isoform
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

```
Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
               |||||||||||||||||||||||||||||||||||||
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 5
AAE02587
ID   AAE02587 standard; protein; 697 AA.
XX
AC   AAE02587;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK).
XX
KW   Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
```

KW therapy; Alzheimer's disease; antialzheimer's.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US026080.
XX
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
DR N-PSDB; AAD06745.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
PS Example 6; Page 143-145; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human APP695-KK. This
CC sequence contains two carboxy-terminal lysine residues
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
```

```
Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 6
AAU06609
ID   AAU06609 standard; protein; 697 AA.
XX
AC   AAU06609;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-KK; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 696. .697
FT                   /note= "2 Extra Lys residues added compared to wild-type
FT                   APP695"
XX
PN   WO200149098-A2.
XX
```

PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000798.
XX
PR 09-MAY-2001; 2001WO-IB000798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
DR N-PSDB; AAS11523.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 6; Page 144-146; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence is the human APP695 mutant, APP695-
CC KK which has 2 extra Lys residues added at the C-terminus compared to the
CC wild-type APP695. The mutation alters the specificity of the APP gamma-
CC secretase activity and increases the rate of processing of the amyloid
CC Abeta peptide
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 7
ABB78596
ID   ABB78596 standard; protein; 697 AA.
XX
AC   ABB78596;
XX
DT   16-JUL-2002  (first entry)
```

XX

DE Human APP695-KK protein sequence SEQ ID NO:16.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowkski MJ, Gurney M;

XX

DR WPI; 2002-397167/43.
DR N-PSDB; ABL52463.

XX

PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.

XX

PS Example 6; Page 114-116; 182pp; English.

XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP695-KK, which is
CC given in an example from the present invention

XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 5; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 8

AAY88430
ID AAY88430 standard; protein; 697 AA.
XX
AC AAY88430;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP695-VF-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP695-VF-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15667.
XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Claim 133; Page 148-153; 183pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease
XX
SQ Sequence 697 AA;

  Query Match 99.9%; Score 3646; DB 3; Length 697;

```
  Best Local Similarity   99.9%;  Pred. No. 3.3e-253;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
AAU07210
ID   AAU07210 standard; protein; 697 AA.
XX
AC   AAU07210;
```

XX

DT 24-OCT-2001 (first entry)

XX

DE Human beta-amyloid protein precursor, APP695-VF-KK.

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP695-VF-KK.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
FT Misc-difference 642
FT /note= "Wild type Val substituted by Phe"

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000797.

XX

PR 09-MAY-2001; 2001WO-IB000797.

XX

PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502548/55.
DR N-PSDB; AAS11710.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX

PS Example 8; Page 150-152; 185pp; English.

XX

CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the

CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of human amyloid
CC protein precursor, APP695-VF-KK, used in the method of the invention
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.3e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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                    ||||||||||||||||||||||||||||||||||||
Db          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
AAE10637
ID   AAE10637 standard; protein; 697 AA.
XX
AC   AAE10637;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.
XX
KW   Human; aspartyl protease 1; Asp1; amyloid precursor protein;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   APP695-VF-KK; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted with Phe"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-00023315.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   N-PSDB; AAD17873.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Example 8; Page 120-122; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
```

CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic acti0ity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence is
CC obtained by the addition of two lysine residues (KK motif) at the C-
CC terminus of App695-VF isoform which is generated by the London mutation
CC in APP695, where Val at position 642 is replaced with Phe. APP695-VF-KK
CC isoform is useful for assaying the beta-secretase activity of human
CC aspartyl protease 2a (hu-Asp2a) protein
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.3e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                    ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
                    |||||||||||||||||||||||||||||||||||
Db          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 11
AAE06867
ID AAE06867 standard; protein; 697 AA.
XX
AC AAE06867;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.
XX
KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Misc-difference 642
FT   /note= "Wild type Val substituted with Phe"
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
DR N-PSDB; AAD13029.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity.
XX
PS Example 8; Page 150-152; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is modified human amyloid precursor protein 695-VF-
CC KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is obtained by addition
CC of two Lys residues (KK motif) at the C-terminal end of APP695-VF
CC isoform. APP695-VF isoform is obtained by London V-F mutation in APP695
CC isoform, where Val at position 642 is replaced with Phe. APP695-VF-KK
CC isoform is useful for assaying the beta-secretase activity of human
CC aspartyl protease 2a (Hu-Asp2a) protein
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.3e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
```

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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 12
AAE02589
ID   AAE02589 standard; protein; 697 AA.
XX
AC   AAE02589;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
XX
KW   Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;
KW   APP695-VF-KK; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
```

DR N-PSDB; AAD06747.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
PS Example 8; Page 149-151; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human APP695-VF-KK. This
CC sequence is characterised by a V to F alteration at position 642 and
CC contains two carboxy-terminal lysine residues
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.3e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
```

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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 13
AAU06611
ID   AAU06611 standard; protein; 697 AA.
XX
AC   AAU06611;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-VF-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted by Phe"
FT   Misc-difference 696. .697
FT                   /note= "2 Extra Lys residues added compared to wild-type
FT                   APP695"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000798.
XX
PR   09-MAY-2001; 2001WO-IB000798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11525.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
```

PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 8; Page 150-152; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence is the human APP695 mutant, APP695-
CC VF-KK which has 2 extra Lys residues added at the C-termunis compared to
CC APP695-VF (the London mutation). The mutation alters the specificity of
CC the APP gamma-secretase activity and increases the rate of processing of
CC the amyloid Abeta peptide
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.3e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                    |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
                    |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 14
ABB78598
ID   ABB78598 standard; protein; 697 AA.
XX
AC   ABB78598;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-VF-KK protein sequence SEQ ID NO:20.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW   amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
```

PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
DR N-PSDB; ABL52465.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Example 8; Page 120-122; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP695-VF-KK, which
CC is given in an example from the present invention
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 5; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.3e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 15
ADB87314
ID   ADB87314 standard; protein; 740 AA.
XX
AC   ADB87314;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human amyloid A4 precursor (APP) Swedish mutant protein with tags.
XX
KW   amyloid precursor protein; APP; amino acid tag; gamma-secretase;
KW   alpha-secretase; beta-secretase; C-terminal cleavage product; gammaCTF;
KW   presenilin 1; Alzheimer's disease; beta-amyloid; senile plaque;
KW   secretase inhibitor; APP biosynthesis; APP activity; human;
KW   amyloid A4 precursor; Swedish mutant; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

FT Misc-difference 595
FT /note= "Wild-type Lys substituted by Asn"
FT Misc-difference 596
FT /note= "Wild-type Met substituted by Leu"
FT Cleavage-site 645. .646
FT /note= "Cleavage of the APP protein between these two
FT residues by gamma-secretase produces gammaCTF"
FT Region 718. .731
FT /label= V5_epitope_tag
FT Region 735. .740
FT /label= Polyhistidine_tag
XX
PN WO2003064681-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-GB000433.
XX
PR 31-JAN-2002; 2002GB-00002276.
XX
PA (EISA) EISAI LONDON RES LAB LTD.
XX
PI Lucas FR, Taylor J;
XX
DR WPI; 2003-663492/62.
XX
PT New protein comprising an amyloid precursor protein and an amino acid
PT tag, useful for screening or identifying therapeutic compounds,
PT particularly secretase inhibitors, useful for the treatment of diseases
PT e.g. Alzheimer's disease.
XX
PS Claim 4; Page; 24pp; English.
XX
CC This invention relates to a novel protein which comprises an amyloid
CC precursor protein (APP) and an amino acid tag. The present invention also
CC relates to assays for measuring gamma-secretase activity and/or
CC simultaneously measuring alpha, beta or gamma-secretase activity which
CC involve utilising the stabilisation of the gamma-secretase C-terminal
CC cleavage product of APP (gamma C-terminal fragment of APP; gammaCTF).
CC GammaCTF is generated by the action of gamma-secretase/presenilin 1, an
CC important enzyme in Alzheimer's disease. GammaCTF is the sister product
CC of beta-amyloid which is produced by the same process and accumulates in
CC senile plaques in Alzheimer's disease. The protein or the methods of the
CC invention may be useful for screening a test compound for its ability to
CC modulate alpha, beta or gamma-secretase activity. In particular, the
CC protein or methods are useful for screening or testing secretase
CC inhibitors, and differentiating such inhibitors from agents that act
CC indirectly, for example interface with normal APP biosynthesis and
CC activity. The amino acid tag of the new protein is useful for the
CC stabilisation of gamma-secretase cleavage products of APP. Specifically,
CC the protein or methods may be useful for screening or identifying
CC therapeutic compounds or compositions for the treatment of diseases such
CC as Alzheimer's disease. The present sequence is that of the Swedish
CC mutant human amyloid A4 precursor (APP) of the invention, tagged with a
CC V5 epitope tag and a polyhistidine tag, which was expressed in KEK293
CC cells during the exemplification of the invention. Note: This sequence
CC does not appear in the specification but was created by the indexer from

CC information given.
XX
SQ Sequence 740 AA;

Query Match 99.9%; Score 3646; DB 7; Length 740;
Best Local Similarity 100.0%; Pred. No. 3.6e-253;
Matches 696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 52.6667 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:08:40 ; Search time 17 Seconds
(without alignments)
2116.665 Million cell updates/sec

Title: US-09-806-194A-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3651	100.0	697	4	US-09-548-367D-16	Sequence 16, Appl
3	3651	100.0	697	4	US-09-551-853D-16	Sequence 16, Appl
4	3646	99.9	697	4	US-09-548-372D-20	Sequence 20, Appl
5	3646	99.9	697	4	US-09-548-367D-20	Sequence 20, Appl
6	3646	99.9	697	4	US-09-551-853D-20	Sequence 20, Appl
7	3643	99.8	697	4	US-09-548-372D-18	Sequence 18, Appl
8	3643	99.8	697	4	US-09-548-367D-18	Sequence 18, Appl
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18	3641	99.7	695	4	US-09-551-853D-10	Sequence 10, Appl
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24	3635	99.6	694	1	US-08-339-152A-18	Sequence 18, Appl
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30	3629	99.4	695	1	US-08-371-930-27	Sequence 27, Appl
31	3629	99.4	695	5	PCT-US94-01712-27	Sequence 27, Appl
32	3617	99.1	695	1	US-08-339-152A-30	Sequence 30, Appl
33	3612	98.9	753	4	US-09-548-372D-61	Sequence 61, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 16, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-09-548-372D-16

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  Matches 697; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-09-548-367D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-266;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-09-551-853D-16
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Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-266;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 4
US-09-548-372D-20
; Sequence 20, Application US/09548372D

; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-20

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.4e-266;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 5
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-20

  Query Match             99.9%;  Score 3646;  DB 4;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 3.4e-266;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
               |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
               |||||||||||||||||||||||||||||||||||||
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 6
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18

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;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-20

  Query Match             99.9%;  Score 3646;  DB 4;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 3.4e-266;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                    |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
                    |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-18

  Query Match             99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.7e-266;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||| :||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
                |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 8
US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 99.8%; Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%; Pred. No. 5.7e-266;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-18

  Query Match             99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.7e-266;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
US-08-123-702-2
; Sequence 2, Application US/08123702
; Patent No. 5604131
;  GENERAL INFORMATION:
;    APPLICANT:  Wadsworth, Samuel
;    APPLICANT:  Snyder, Benjamin
;    APPLICANT:  Reddy, Vermuri, B.
;    APPLICANT:  Wei, Chamer
;    TITLE OF INVENTION:  A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
;    TITLE OF INVENTION:  Containing a Genomic DNA Insert of the KI and OX-2
Regions
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  GA
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/123,702
;      FILING DATE:  17-SEPT-1993
```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: TSI121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-702-2

Query Match 99.7%; Score 3641; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 8e-266;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
                    |||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 11
US-08-104-165-1
; Sequence 1, Application US/08104165
; Patent No. 5877015
;  GENERAL INFORMATION:
;    APPLICANT:  HARDY, John Anthony
;    APPLICANT:  GOATE, Alison Mary
;    APPLICANT:  MULLAN, Michael John
;    APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;    APPLICANT:  OWEN, Michael John
;    TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/104,165
;      FILING DATE:  21-JAN-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  9101307.8
;      FILING DATE:  21-JAN-1991
;      APPLICATION NUMBER:  9118445.7
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  16163-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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; MOLECULE TYPE: protein
US-08-104-165-1

Query Match 99.7%; Score 3641; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 8e-266;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 12

US-08-464-250-1
; Sequence 1, Application US/08464250
; Patent No. 6107542
; GENERAL INFORMATION:
;   APPLICANT: HARDY, John Anthony
;   APPLICANT: GOATE, Alison Mary
;   APPLICANT: MULLAN, Michael John
;   APPLICANT: CHARTIER-HARLIN, Marie-Christine
;   APPLICANT: OWEN, Michael John
;   TITLE OF INVENTION: Test and Model for Alzheimer's Disease
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: 379 Lytton Avenue
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: US
;   ZIP: 94301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/464,250
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/104,165
;   FILING DATE: 21-JAN-1992
;   APPLICATION NUMBER: 9101307.8
;   FILING DATE: 21-JAN-1991
;   APPLICATION NUMBER: 9118445.7
;   FILING DATE: 28-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Liebeschuetz, Joe
;   REGISTRATION NUMBER: 37,505
;   REFERENCE/DOCKET NUMBER: 16163-000100
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 326-2400
;   TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 695 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-464-250-1

  Query Match   99.7%; Score 3641; DB 3; Length 695;
  Best Local Similarity   100.0%; Pred. No. 8e-266;
  Matches 695; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 13
US-08-464-250-1
; Sequence 1, Application US/08464250
; Patent No. 6300540
;   GENERAL INFORMATION:
;        APPLICANT: HARDY, John Anthony
;                   GOATE, Alison Mary
;                   MULLAN, Michael John
;                   CHARTIER-HARLIN, Marie-Christine
;                   OWEN, Michael John
;        TITLE OF INVENTION: Test and Model for Alzheimer's Disease
;        NUMBER OF SEQUENCES: 44
```

```
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Townsend and Townsend Khourie and Crew
;              STREET: 379 Lytton Avenue
;              CITY: Palo Alto
;              STATE: California
;              COUNTRY: US
;              ZIP: 94301
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy Disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/08/464,250
;              FILING DATE: 05-Jun-1995
;              CLASSIFICATION: 435
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/104,165
;              FILING DATE: 21-JAN-1992
;              APPLICATION NUMBER: 9101307.8
;              FILING DATE: 21-JAN-1991
;              APPLICATION NUMBER: 9118445.7
;              FILING DATE: 28-AUG-1991
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Liebeschuetz, Joe
;              REGISTRATION NUMBER: 37,505
;              REFERENCE/DOCKET NUMBER: 16163-000100
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 326-2400
;              TELEFAX: (415) 326-2422
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 695 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-464-250-1

  Query Match             99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8e-266;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 14
US-09-458-481B-7
; Sequence 7, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
;  APPLICANT: KUMAR, Vijaya B.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
;  FILE REFERENCE: 16153-9250
;  CURRENT APPLICATION NUMBER: US/09/458,481B
;  CURRENT FILING DATE:  1999-12-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Monkey
US-09-458-481B-7

  Query Match             99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8e-266;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 15
US-09-458-481B-8
; Sequence 8, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
; APPLICANT: KUMAR, Vijaya B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
; FILE REFERENCE: 16153-9250

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;  CURRENT APPLICATION NUMBER: US/09/458,481B
;  CURRENT FILING DATE:  1999-12-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-458-481B-8

  Query Match            99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 8e-266;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Search completed: May 24, 2004, 15:16:04
Job time : 19 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:06:00 ; Search time 14.3333 Seconds
(without alignments)
4677.593 Million cell updates/sec

Title: US-09-806-194A-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3641	99.7	695	1	A49795	Alzheimer's diseas
2	3590.5	98.3	770	1	QRHUA4	Alzheimer's diseas
3	3544	97.1	695	2	S00550	Alzheimer's diseas
4	3519	96.4	695	2	A27485	Alzheimer's diseas
5	3103	85.0	747	2	JH0773	Alzheimer's diseas
6	2105	57.7	484	4	A32761	hypothetical Alzhe
7	1728	47.3	763	2	A49321	amyloid beta (A4)
8	1716	47.0	765	2	S42880	amyloid precursor-
9	1704	46.7	751	2	A49974	beta-amyloid precu
10	1185	32.5	653	2	A46362	amyloid precursor-
11	1143	31.3	511	2	JC1404	CDEI-box DNA-bindi
12	817.5	22.4	686	2	T15795	hypothetical prote
13	747	20.5	886	2	A32758	beta-amyloid-like

14	706	19.3	246	2	S38344	CDEI-binding prote
15	411	11.3	82	2	PQ0438	Alzheimer's diseas
16	296.5	8.1	191	2	A35981	sperm membrane pro
17	283	7.8	57	2	E60045	Alzheimer's diseas
18	283	7.8	57	2	F60045	Alzheimer's diseas
19	283	7.8	57	2	G60045	Alzheimer's diseas
20	283	7.8	57	2	D60045	Alzheimer's diseas
21	283	7.8	57	2	A60045	Alzheimer's diseas
22	283	7.8	57	2	B60045	Alzheimer's diseas
23	217	5.9	42	2	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	I51116	NF-180 - sea lampr
25	186	5.1	5170	2	T15348	hypothetical prote
26	185.5	5.1	407	1	EDBEQ3	immediate-early pr
27	185.5	5.1	993	2	S49461	synaptonemal compl
28	182	5.0	522	2	T32444	hypothetical prote
29	175.5	4.8	802	1	S48529	NAB3 protein - yea
30	175.5	4.8	1188	2	T46608	zinc finger protei
31	174.5	4.8	464	2	H90279	microtubule bindin
32	174.5	4.8	884	2	T20405	hypothetical prote
33	174	4.8	579	2	JH0820	160K golgi antigen
34	174	4.8	1087	2	T30330	gelsolin-related p
35	173.5	4.8	793	1	JH0628	caldesmon - human
36	172	4.7	771	1	A33430	h-caldesmon - chic
37	172	4.7	784	2	PN0009	neurofilament trip
38	172	4.7	1182	2	T30189	myelin transcripti
39	171	4.7	1271	2	A45555	glutamate rich pro
40	170	4.7	1948	2	S00485	gene 11-1 protein
41	169.5	4.6	298	1	TPHUTC	troponin T, cardia
42	169.5	4.6	721	2	S29795	hypothetical prote
43	169	4.6	885	2	G71608	ATP-dept. acyl-CoA
44	169	4.6	1187	2	T46637	transcription fact
45	168.5	4.6	675	2	T03744	myoD protein inhib

ALIGNMENTS

RESULT 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing

```
  Query Match             99.7%;  Score 3641;  DB 1;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-184;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 2
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
```

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.

A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
A;Reference number: A44017; MUID:93035397; PMID:1415269

A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.;
Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a
cell-surface receptor.
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the
cerebrovascular and the neuritic plaque amyloid peptides.
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain
amyloid of Alzheimer's disease.
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop,
P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage
near the Alzheimer locus.
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang,
J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
EMBO J. 7, 949-957, 1988

A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 98.3%; Score 3590.5; DB 1; Length 770;
Best Local Similarity 90.1%; Pred. No. 2.1e-181;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
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Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
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Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
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Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
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Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```

RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.

A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 97.1%; Score 3544; DB 2; Length 695;
Best Local Similarity 97.3%; Pred. No. 5.3e-179;
Matches 676; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| |||||||||||||||||||||||:|||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||::|||||||||||||||||||||| |||||||||||||:||||
Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||:|||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||:|| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match   96.4%; Score 3519; DB 2; Length 695;
  Best Local Similarity   96.8%; Pred. No. 1.1e-177;
  Matches 673; Conservative   5; Mismatches   17; Indels   0; Gaps   0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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                |||  |||||||||| |||||||||||||||||||||||:||||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               |||  |||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               |||||||||||||:|||||||||||||| |||||||| |||||||||||||:||||
Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWVGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               |||||||  |||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               |||||||||||||||||||||||||||||||||| |||||  |||||||||  |||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLDLENYIIALQAVPPRPHHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKATQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               |||||||  || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                ||||:||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
               |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
```

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992

A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 85.0%; Score 3103; DB 2; Length 747;
Best Local Similarity 81.0%; Pred. No. 8.8e-156;
Matches 598; Conservative 35; Mismatches 41; Indels 64; Gaps 5;

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Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75
Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253
Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQPDEEEEVVEVEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTESVEEVVR---------------------------- 288
Db        250 AEEEPEEPYEEATERTTSIATTTTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVTE 309

Qy        289 --------------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377
Db        370 KAKERLEGKHREKMSEVMKEWEEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELFQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609
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Qy        558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
              ||||||||||||||||||||||||||||||||||||||:|:|||: ||||||||||||
Db        610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677
              |:||||||||||||||||||||||||||||||||||:||||||||||||||||||:||
Db        670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHHGVVEVDAAVTPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||
Db        730 QQNGYENPTYKFFEQMQN 747
```

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C;Accession: A32761
R;de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted protein.
A;Reference number: A32761; MUID:89346754; PMID:2569763
A;Accession: A32761
A;Molecule type: mRNA
A;Residues: 1-484 <DES>
A;Cross-references: GB:M28373
A;Note: the authors translated the codon ATG for residue 433 as Leu
C;Comment: This is the hypothetical translation of a sequence believed to contain cloning artifacts.
C;Keywords: cloning artifact

Query Match 57.7%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 1.5e-103;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;

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Qy         80 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 60

Qy        140 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 120

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAE 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAE 180

Qy        260 EPYEEATERTTSIATTTTTTTESVEEVVR------------------------------ 288
              ||||||||||||||||||||||||||||
Db        181 EPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPF 240

Qy        289 -------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 323
                                        :||||||||||||||||||||||||||||||||
Db        241 FYGGCGGNRNNFDTEEYCMAVCGSAIPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 300
```

```
Qy        324 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 360

Qy        384 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 420

Qy        444 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 487
              |||||||||||||||||||||||||||||||||||||||||||||
Db        421 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 464
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RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
N;Alternate names: CDEI-binding protein
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49321; S34644; S40519
R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, D.C.
Biochemistry 32, 4481-4486, 1993
A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a multigene family.
A;Reference number: A49321; MUID:93250009; PMID:8485127
A;Accession: A49321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <SPR>
A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor like protein.
A;Reference number: S34644
A;Accession: S34644
A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.; Neve, R.L.; Tanzi, R.E.
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's associated amyloid beta protein precursor.
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2

A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.3%; Score 1728; DB 2; Length 763;
Best Local Similarity 47.1%; Pred. No. 1.7e-83;
Matches 372; Conservative 112; Mismatches 165; Indels 140; Gaps 20;

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Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | ||||   || || :         |||    :||||||||||:||||:|:| |||: ||
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:| :||| :||||||:|||||||||:|||| |:| |||:| :||||:   || |::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| ||||:||:| |:|||:||| | ||||| || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||| :   :|   : |||:       : :  |  ||  |  :|    |:
Db        193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEDEEEDYDVYKSEFPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTTSIATTTTTTTES 282
              :|:  | |  :||||:|:|:|| |: :  |          |  ||  :    :    |
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV-------------------------------------------------------VRVP 290
              |: |                                                       :|
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 350
               |   | | || | ||  |:|||| |||||:|| :|| || :| :|||||| |||||||
Db        366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 410
              |::: :|||||  |::||:|||:|:|||||||:||||||||||||:|||||: |||: ||
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
              ||  :   |::|||||| ||| ||::|::||  |||:||||::|||||| || || ||||
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSL 544

Qy        471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVE 530
              |||| || ||:|||:|:|||||::: |:|  |  |::||  |
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISETPVDVR 587

Qy        531 LLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN----- 585
                 |: | | ::: |:| |     ||  |||    | :|     :  : |||:
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL 635

Qy        586 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKG 625
              |  ||    |: |:|     |   :|  ::::| || ||                  :
```

```
Db        636 IGAEEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSS 693

Qy        626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENP 685
              |:|||:|  | |||||||:||||:|:|| :| ||:|||| :|||||||:||| :||||||
Db        694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENP 753

Qy        686 TYKFFEQMQ 694
              ||| |||| |
Db        754 TYKYLEQMQ 762
```

RESULT 8
S42880
amyloid precursor-like protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42880; S47528
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A;Description: Complete nucloetide ad deduced amino acid sequence of rat amyloid precursor-like protein 2 (Aplp2/Apph): Two amino acids length difference to human and murine homologues.
A;Reference number: S42880
A;Accession: S42880
A;Molecule type: mRNA
A;Residues: 1-765 <SAN>
A;Cross-references: EMBL:X77934
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor-like protein 2 (APLP2/APPH): two amino acids length difference to human and murine homologues.
A;Reference number: S47528; MUID:94368849; PMID:8086458
A;Accession: S47528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <SA2>
A;Cross-references: EMBL:X77934
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing
F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match   47.0%; Score 1716; DB 2; Length 765;
  Best Local Similarity   46.2%; Pred. No. 7.4e-83;
  Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;

```
Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   || |  :         |||    :||||||||||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :||||||:||||||||:|||||| | :||:| :|||::  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| |||||: |:| |||||:||| |  |||| || |  :   |: ||||||||:
```

```
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 233
              |:| | |:|||| : :||: | : ||:: :      : ||| | ||       |:
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTTSIATTTTTTTESVEEVV 287
               |  :|:| :::|::|:|:|| |: :  |:         |  |  ::  | : : :   |
Db        249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R-----------------------------------------------------------VPT 291
              :                                                           :|
Db        309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 368

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||||| ||||||||
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ::: :|||||  |::||:|||:|:|||||||:||||||||||||:|||||: |||: |||
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |  :   |::|||||| ||| ||::|::||  |||:||||::|||||| || || |||||
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| || ||:|||:|:|||||:::       |:|          |    |::|    |
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN-----I 586
              |: | | ::: |:| |     |: :|||    | :|     :  : |||:       |
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELYHPM--KKGSGMAEQDGGLI 638

Qy        587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKGA 626
              ||    |: |||     |   :|  ::::| || ||                   :  |
Db        639 GAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSA 696

Qy        627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPT 686
              :|||:|  | |||||||:||||:|:|| :| ||:|||   :|||||||:||| :||||||
Db        697 LIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPT 756

Qy        687 YKFFEQMQ 694
              ||: ||||
Db        757 YKYLEQMQ 764
```

RESULT 9
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49974
R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994

A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid precursor protein (APP).
A;Reference number: A49974; MUID:94132029; PMID:8300594
A;Accession: A49974
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-751 <SLU>
A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.7%; Score 1704; DB 2; Length 751;
Best Local Similarity 45.9%; Pred. No. 3.1e-82;
Matches 363; Conservative 113; Mismatches 159; Indels 156; Gaps 20;

```
Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   || |  :         |||    :||||||||||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :||||||:||||||||:|||||| | :||:| ::|||:  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| ||||| |:| |||||:||| |  |||: || |  :   |: |||||||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231
              |:| | |:|||| :  :||:  | : ||::          |  |  ||  :: :|   |
Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEAD-DDEDDEDGDEVEEE--------------AEEPYEEATERTTSIATTT 276
               :: :  |  || ::||:|:|:|| |:               | | | ::| | |
Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNEENPTEPSSEGTIS----- 298

Qy        277 TTTTESVEEV---------------------------------------------------- 286
                  | | :|
Db        299 --DKEIVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYC 356

Qy        287 -----VRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
                    :| |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||||
Db        357 MAVCKAMIPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEA 415

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
              | ||||||| ::: :|||||  |::||:|||:|:|||||||:||||||||||||:|||||
Db        416 ELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENY 475

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
              : |||: ||||  :   |::|||| ||| ||::|::||  |||:||||::|||||| |
Db        476 LAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHV 535

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
              | || |||||||| || ||:|||:|:||||::        |:|          |    |
Db        536 IEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSS 578
```

```
Qy        522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
              ::|    | :     |  :    | | |     |: :|||           |:  : |
Db        579 ISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQDG- 621

Qy        582 GLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------N 623
              ||   : : | |: |||     |   :|  ::::| || ||                 :
Db        622 GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFSLS 679

Qy        624 KGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYE 683
               |:|||:|  | |||||||:||||:|:|| :| ||:|||| :|||||||:||| :|||
Db        680 SNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYE 739

Qy        684 NPTYKFFEQMQ 694
              |||||: ||||
Db        740 NPTYKYLEQMQ 750
```

RESULT 10
A46362
amyloid precursor-like protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46362
R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
A;Title: Identification of a mouse brain cDNA that encodes a protein related to
the Alzheimer disease-associated amyloid beta protein precursor.
A;Reference number: A46362; MUID:93066322; PMID:1279693
A;Accession: A46362
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-653 <WAS>
A;Experimental source: brain
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: transmembrane protein

  Query Match   32.5%; Score 1185; DB 2; Length 653;
  Best Local Similarity   38.6%; Pred. No. 5e-55;
  Matches 270; Conservative 121; Mismatches 231; Indels   78; Gaps   17;

```
Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
              :|| |:|||| |  |   | | :   |      |:|  |||| :| ::: |:|: ||  :
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
              : |:   : :|:||:::|||| |  | :| | : :: ||   |     |||  |:|: ||
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
               |||||:|||||: |:|||||||| ||:    |  |:| || :   ||  ||||||| |:
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
              |||||:||||    : |    | :  :  |  ||     |:| ||       ||||
```

```
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
              :   |   :    :| ||| ||     :  |  : :  | |          ||
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              | || |   ||:  ||  | :|| || :   ::::|||||  |: |:|||||||::|:
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              :|||  :::||:: : |||:|||||  || |::||:|| ||| :: |||  ||:   |
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |::|:|||||:::|||:|::||  |||:|| |:| || |||:|| ||||||| ||   |
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
              :|:|:: :: |||          ||  :    :    || :| | :| |
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
                   |||             |:: :|    |   :| | :  |     |   : : :
Db        511 ----GSLQP------------PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551

Qy        597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKKQ 652
                     |:  |    |:         | :: |: ||:: |    ::||::|::| |||
Db        552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKP 611

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
              | :| |||||||  :| ||: | ::|::|||||||:| |:
Db        612 YGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651
```

RESULT 11
JC1404
CDEI-box DNA-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C;Accession: JC1404
R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
A;Title: A murine sequence-specific DNA binding protein shows extensive local similarities to the amyloid precursor protein.
A;Reference number: JC1404; MUID:93129193; PMID:1482349
A;Accession: JC1404
A;Molecule type: mRNA
A;Residues: 1-511 <VID>
C;Comment: This protein plays an important role in the early development of the mouse.
C;Keywords: DNA binding; transmembrane protein

Query Match 31.3%; Score 1143; DB 2; Length 511;
Best Local Similarity 45.8%; Pred. No. 6e-53;
Matches 253; Conservative 92; Mismatches 128; Indels 80; Gaps 16;

```
Qy        174 CGIDKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE- 230
              ||:|:| | |:|||| : :||: | : ||:: | | || :: :|
Db          6 CGVDQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEF 56

Qy        231 --EEEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTT 279
                | :: : | || ::|||:|:|:|| |: : : | | | | :: | :
Db         57 PTEADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS 114

Qy        280 TESVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 339
               : :  |:|| |  | | || | ||  |:|||| |||||:|| :|| || :| :|||
Db        115 DKEIVHDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWE 173

Qy        340 EAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALE 399
              ||| ||||||| ::: :||||| |::||:|||:|:|||||||:|||||||||||||:|||
Db        174 EAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALE 233

Qy        400 NYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHL 459
              ||: |||: |||| : |::|||| ||| ||::|::|| |||:||||::|||||||
Db        234 NYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHL 293

Qy        460 RVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALM 519
               || || |||||||| || ||:|||:|:|||||::: |:| |
Db        294 HVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFT 336

Qy        520 PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRP 579
               |::|  | :  | :  | | |  |: :|||  |:  :
Db        337 SSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQD 380

Qy        580 GSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---------------- 622
              | ||  : : | |: |||  |  :|  ::::| || ||
Db        381 G-GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFS 437

Qy        623 -NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNG 681
               :  |:|||:|  | |||||||:||||:|:|| :| ||:|||| :|||||||:||| :|
Db        438 LSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHG 497

Qy        682 YENPTYKFFEQMQ 694
              |||||||: ||||
Db        498 YENPTYKYLEQMQ 510
```

RESULT 12
T15795
hypothetical protein C42D8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C;Accession: T15795; A49414
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8.
A;Reference number: Z18405
A;Accession: T15795
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-686 <HAL>
A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1;
GSPDB:GN00028; CESP:C42D8.8

A;Experimental source: strain Bristol N2; clone C42D8
R;Daigle, I.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A;Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the human beta-amyloid protein precursor.
A;Reference number: A49414; MUID:94089766; PMID:8265668
A;Accession: A49414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-686 <DAI>
A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
C;Genetics:
A;Gene: CESP:C42D8.8
A;Map position: X
A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 22.4%; Score 817.5; DB 2; Length 686;
Best Local Similarity 29.1%; Pred. No. 1.1e-35;
Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :: || : :| | |  |   |          | :|  ||  | :|  : | | :|
Db          6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||   |  ||:||:: || : |||:|| :  |:| :||:     ||   | | || |: |
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN------LHDYGMLLPC 174
              || |:|| ||  |:| |    | |  : ||   | : |  | :       :  : :| ||
Db        123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
             :| | ||||||||    :|  :  | ::
Db        183 ALDMFTGVEFVCCP----NDQTNKTDVQKTK---------------------------- 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
               |:|: ||||||   |:  ||::|  ||
Db        210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE---------------------------- 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
              | : | | :     |||  |:||: |:: |||::: :||:|| :      |::||: |
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
              |  :|   |    ||: | |||:|    |:::   |  ||:||||:::| |  :|  ||
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
                   |    |   || |:|||:||| |||  : |:   | |:||  :  |:  || |
Db        355 THVNKPNKHSVLQSLKAYIRAEEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              |:| :|::| : |          ||   :: :|||   :  |    |  |  :| :   |
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Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANT---ENEVEP 564
                  |   |: |    :     ::||     | ::   ::    |     |   : :|:
Db        471 NAKLDVKAPTTTAKPVKETDNAKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy        565 VDARP--------------------AADRGLTTRPGSGLTNIKTEE-----ISEVKMDA 598
                || :|                        |        |  |: :::|     | |:::|
Db        531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
                |         :|||        ||:   |   |        ::   :  | | |    :
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
                :      | :|||   ||||||:: || ||||||| ||:
Db        643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683
```

RESULT 13
A32758
beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998
C;Accession: A32758
R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989
A;Title: A Drosophila gene encoding a protein resembling the human beta-amyloid protein precursor.
A;Reference number: A32758; MUID:89184650; PMID:2494667
A;Accession: A32758
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <ROS>
A;Cross-references: GB:J04516; NID:g158371; PID:g158372
C;Genetics:
A;Gene: FlyBase:Appl
A;Cross-references: FlyBase:FBgn0000108
C;Keywords: transmembrane protein

Query Match 20.5%; Score 747; DB 2; Length 886;
Best Local Similarity 25.5%; Pred. No. 7.8e-32;
Matches 233; Conservative 127; Mismatches 288; Indels 264; Gaps 29;

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Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
              ||| : |   |:     | | : |     |||||: |  |::     : : |:| :| |
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK 63

Qy         59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
                ||:  |  :| ||:: ||   |||:||::    |  ||::|     :||    ::
Db         64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
             |:||| | | |||||||: | | |       |   : |:      | |:   :  : |||
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP-----------------------------LAEESDNVD---SA 199
```

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                |||| | ||||||||                                    : :| |: |   |
Db        183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELMNDEDDSNDSNYSK 242

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV----------------------AEV 237
                || ||| |      | |   | :::   ||:|                          ||
Db        243 DANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAEY 296

Qy        238 EE-EEADDDEDDEDGDEVEEEAEEPY--------------------------EEATERT 269
                :  || |: |:|  | | | | |  :                          |:|  ::
Db        297 DSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVKS 356

Qy        270 TSIATTTTTTTESVEEVV----------RVPTTAASTPDAVDKYLETPGDENEHAHFQK 318
                 |: :|   :  :   |              |:||  |    | |        ||  ::
Db        357 ESVTSTPQLSASAAAFVAANSGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYKV 413

Qy        319 AKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQEA 371
                :::|||  |||:::::||::| : | : :::  || ||       :   ||  |::||:|
Db        414 SQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEEG 473

Qy        372 ANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQ 431
                  |: ||   |  || | :| |:| |:  |  ||   ||   ||   |:| :||  |||
Db        474 NAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRA 533

Qy        432 HTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI---- 483
                | | |: | :    |   : ||  | : :  |  |   :|||:::|   | :: :|
Db        534 HALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQLM 593

Qy        484 ---------QDEV-------------------------------------------------- 487
                       :|::
Db        594 NDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAAE 653

Qy        488 -----DELLQKEQNYSDDVLANMISE----------------------PRISYGNDALM 519
                   :| |: |    ||:| : ::|                      |    | || :
Db        654 REKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAAL 713

Qy        520 -----PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRG 574
                   |:|  ||:         |  | | :    :|  :|       | |     |  |
Db        714 VTAANPNLETTKS---------EKDLSDTE----YGEATVSTTKVQTVLPTVDDDAVQRA 760

Qy        575 LTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GA 626
                :     :         ::  : : : :|   ::: |::  |     ||:   : |
Db        761 VEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRNV 811

Qy        627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQQ 679
                   |   |: :   : : : : | :   | |  | :|||  ||       ||: :  ||
Db        812 YFTLSFAGIALMAAVFVGVAVAKWRTSRSPHAQGFIEVDQNVTTHHPIVREEKIVPNMQI 871

Qy        680 NGYENPTYKFFE 691
                |||||||||:||
Db        872 NGYENPTYKYFE 883
```

RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996

C;Accession: S38344
R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A;Reference number: S38344; MUID:94032480; PMID:8218408
A;Accession: S38344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <HAN>
A;Cross-references: EMBL:Z22592
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 19.3%; Score 706; DB 2; Length 246;
Best Local Similarity 51.5%; Pred. No. 2.2e-30;
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

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Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   || |  :         |||    :||||||| ||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :||||||:|||||||||:|||||| | :||:| ::|||:  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| ||||| |:| |||||:||| |  |||: || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||   ::  |||                        |  :   ||||
Db        193 DQFHGTEYVCCP---QTKTVDS----------------------DSTMSKEEEEE--- 222

Qy        237 VEEEEADDDED-DEDGDEVEEEAE 259
               ||:| |::|| | |  |   ||:
Db        223 -EEDEEDEEEDYDLDKSEFPTEAD 245
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RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor protein gene.
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 11.3%; Score 411; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        581 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 60

Qy        641 IVITLVMLKKKQYTSIHHGVVE 662
              ||||||||||||||||||||||
Db         61 IVITLVMLKKKQYTSIHHGVVE 82
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Search completed: May 24, 2004, 15:15:01
Job time : 17.3333 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:14:15 ; Search time 38.6667 Seconds
(without alignments)
5027.804 Million cell updates/sec

Title: US-09-806-194A-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	3651	100.0	697	9	US-09-794-927-16	Sequence 16, Appl
2	3651	100.0	697	9	US-09-795-847-16	Sequence 16, Appl
3	3651	100.0	697	9	US-09-794-743-16	Sequence 16, Appl
4	3651	100.0	697	9	US-09-794-748-16	Sequence 16, Appl
5	3651	100.0	697	9	US-09-794-925-16	Sequence 16, Appl
6	3651	100.0	697	9	US-09-681-442-16	Sequence 16, Appl
7	3651	100.0	697	10	US-09-869-414-16	Sequence 16, Appl
8	3651	100.0	697	10	US-09-548-366-16	Sequence 16, Appl
9	3651	100.0	697	12	US-10-652-927-16	Sequence 16, Appl
10	3651	100.0	697	12	US-10-652-830-16	Sequence 16, Appl
11	3646	99.9	697	9	US-09-794-927-20	Sequence 20, Appl
12	3646	99.9	697	9	US-09-795-847-20	Sequence 20, Appl
13	3646	99.9	697	9	US-09-794-743-20	Sequence 20, Appl
14	3646	99.9	697	9	US-09-794-748-20	Sequence 20, Appl
15	3646	99.9	697	9	US-09-794-925-20	Sequence 20, Appl
16	3646	99.9	697	9	US-09-681-442-20	Sequence 20, Appl
17	3646	99.9	697	10	US-09-869-414-20	Sequence 20, Appl
18	3646	99.9	697	10	US-09-548-366-20	Sequence 20, Appl
19	3646	99.9	697	12	US-10-652-927-20	Sequence 20, Appl
20	3646	99.9	697	12	US-10-652-830-20	Sequence 20, Appl
21	3643	99.8	697	9	US-09-794-927-18	Sequence 18, Appl
22	3643	99.8	697	9	US-09-795-847-18	Sequence 18, Appl
23	3643	99.8	697	9	US-09-794-743-18	Sequence 18, Appl
24	3643	99.8	697	9	US-09-794-748-18	Sequence 18, Appl
25	3643	99.8	697	9	US-09-794-925-18	Sequence 18, Appl
26	3643	99.8	697	9	US-09-681-442-18	Sequence 18, Appl
27	3643	99.8	697	10	US-09-869-414-18	Sequence 18, Appl
28	3643	99.8	697	10	US-09-548-366-18	Sequence 18, Appl
29	3643	99.8	697	12	US-10-652-927-18	Sequence 18, Appl
30	3643	99.8	697	12	US-10-652-830-18	Sequence 18, Appl
31	3641	99.7	695	9	US-09-794-927-10	Sequence 10, Appl
32	3641	99.7	695	9	US-09-795-847-10	Sequence 10, Appl
33	3641	99.7	695	9	US-09-794-743-10	Sequence 10, Appl
34	3641	99.7	695	9	US-09-794-748-10	Sequence 10, Appl
35	3641	99.7	695	9	US-09-794-925-10	Sequence 10, Appl
36	3641	99.7	695	9	US-09-681-442-10	Sequence 10, Appl
37	3641	99.7	695	9	US-09-149-718-2	Sequence 2, Appli
38	3641	99.7	695	10	US-09-869-414-10	Sequence 10, Appl
39	3641	99.7	695	10	US-09-548-366-10	Sequence 10, Appl
40	3641	99.7	695	10	US-09-998-491-1	Sequence 1, Appli
41	3641	99.7	695	12	US-10-652-927-10	Sequence 10, Appl
42	3641	99.7	695	12	US-10-652-830-10	Sequence 10, Appl
43	3641	99.7	695	14	US-10-169-580-3	Sequence 3, Appli
44	3641	99.7	695	14	US-10-357-935-1	Sequence 1, Appli
45	3641	99.7	695	15	US-10-427-208-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-16
; Sequence 16, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-223;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 2
US-09-795-847-16
; Sequence 16, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-795-847-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-223;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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RESULT 3

US-09-794-743-16
; Sequence 16, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-223;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

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RESULT 4
US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-16

  Query Match   100.0%; Score 3651; DB 9; Length 697;
  Best Local Similarity 100.0%; Pred. No. 1.1e-223;
  Matches 697; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 5
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-925-16

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-223;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 6
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881

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;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-681-442-16

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-223;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
US-09-869-414-16
; Sequence 16, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-869-414-16

  Query Match             100.0%;  Score 3651;  DB 10;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-223;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 8
US-09-548-366-16
; Sequence 16, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24

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;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-366-16

  Query Match             100.0%;  Score 3651;  DB 10;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-223;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
US-10-652-927-16
; Sequence 16, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N3
;  CURRENT APPLICATION NUMBER: US/10/652,927
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-10-652-927-16

  Query Match             100.0%;  Score 3651;  DB 12;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-223;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db          241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy          301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy          361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy          421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db          421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy          481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db          481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy          541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db          541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
                    |||||||||||||||||||||||||||||||||||
Db          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 10
US-10-652-830-16
; Sequence 16, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-10-652-830-16

Query Match 100.0%; Score 3651; DB 12; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-223;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
US-09-794-927-20
; Sequence 20, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-927-20

  Query Match           99.9%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 2.4e-223;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 12
US-09-795-847-20
; Sequence 20, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-20

Query Match 99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.4e-223;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 13
US-09-794-743-20
; Sequence 20, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-743-20

  Query Match             99.9%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-223;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 14
US-09-794-748-20
; Sequence 20, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-20

  Query Match 99.9%; Score 3646; DB 9; Length 697;
  Best Local Similarity 99.9%; Pred. No. 2.4e-223;
  Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 15
US-09-794-925-20
; Sequence 20, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-20

Query Match 99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.4e-223;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Search completed: May 24, 2004, 15:28:03
Job time : 40.6667 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:05:00 ; Search time 37.3333 Seconds
(without alignments)
5890.612 Million cell updates/sec

Title: US-09-806-194A-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	3428	93.9	695	13	Q9DGJ8	Q9dgj8 gallus gall
2	3387	92.8	751	13	Q9DGJ7	Q9dgj7 gallus gall
3	3214	88.0	693	13	Q98SG0	Q98sg0 xenopus lae
4	3190	87.4	695	13	Q98SF9	Q98sf9 xenopus lae
5	3188	87.3	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
6	3103	85.0	747	13	Q91963	Q91963 xenopus. ap
7	2964.5	81.2	699	13	O57394	O57394 narke japon
8	2767.5	75.8	569	13	Q9PVL1	Q9pvl1 gallus gall
9	2613	71.6	534	13	O93296	O93296 gallus gall
10	2567	70.3	678	13	Q7ZZT1	Q7zzt1 brachydanio
11	2529	69.3	738	13	Q90W28	Q90w28 brachydanio
12	2487.5	68.1	694	13	Q8UUR9	Q8uur9 brachydanio
13	2339	64.1	612	13	Q9I9E7	Q9i9e7 brachydanio
14	1928	52.8	384	11	Q8BPC7	Q8bpc7 mus musculu
15	1762	48.3	695	4	Q13861	Q13861 homo sapien
16	1749.5	47.9	669	4	Q14662	Q14662 homo sapien
17	1744	47.8	707	11	Q80US7	Q80us7 mus musculu
18	1740	47.7	695	11	Q64348	Q64348 mus musculu
19	1731	47.4	715	11	Q7TT34	Q7tt34 mus musculu
20	1708	46.8	763	11	Q61482	Q61482 mus musculu
21	1704	46.7	751	11	Q60709	Q60709 mus musculu
22	1655	45.3	472	13	Q8UUS0	Q8uus0 brachydanio
23	1350.5	37.0	357	13	Q8UUI8	Q8uui8 brachydanio
24	1301.5	35.6	522	4	Q9BT36	Q9bt36 homo sapien
25	1090	29.9	218	11	Q8BPV5	Q8bpv5 mus musculu
26	1048.5	28.7	523	4	Q14594	Q14594 homo sapien
27	795	21.8	357	13	Q7ZZT2	Q7zzt2 brachydanio
28	771	21.1	239	13	Q8UUI7	Q8uui7 brachydanio
29	577	15.8	113	13	Q8JH58	Q8jh58 chelydra se
30	561	15.4	182	11	Q9CYS4	Q9cys4 mus musculu
31	478	13.1	97	6	Q28673	Q28673 oryctolagus
32	435.5	11.9	140	13	Q800X9	Q800x9 chelydra se
33	393.5	10.8	82	4	Q16019	Q16019 homo sapien
34	389.5	10.7	82	4	Q16014	Q16014 homo sapien
35	387.5	10.6	82	4	Q16020	Q16020 homo sapien
36	376	10.3	79	11	O35463	O35463 cricetulus
37	358.5	9.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
38	335	9.2	208	11	Q8R0R7	Q8r0r7 mus musculu
39	239	6.5	49	6	O97917	O97917 bos taurus
40	196.5	5.4	727	5	Q95TG7	Q95tg7 drosophila
41	196.5	5.4	5303	5	Q9V628	Q9v628 drosophila
42	193	5.3	785	5	Q9GQ82	Q9gq82 drosophila
43	192.5	5.3	556	5	Q95S93	Q95s93 drosophila
44	192.5	5.3	1110	13	Q91255	Q91255 petromyzon
45	191.5	5.2	556	5	Q9V7I9	Q9v7i9 drosophila

ALIGNMENTS

RESULT 1
Q9DGJ8
ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             93.9%;  Score 3428;  DB 13;  Length 695;
  Best Local Similarity   94.0%;  Pred. No. 6.6e-198;
  Matches  655;  Conservative   17;  Mismatches   21;  Indels    4;  Gaps    3;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||||  |||||||  ||||||||||||||||||:||||||||||||:|||||||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||| |||  ||| |:|||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||| ||||||||||||||||||||:||||| ||||||||||||||||||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              ||||||||||||||:||||||:|||||||||||| ||||||:|||||    |:||:  ||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              :|:|||| ||:|||||: || || ||||||||||||||||||||||||||||||||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              ||||||||||||||||||||||||||||||||||:|||||||| ||||||||||
Db        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNM 418
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Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPA 478

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEF 538

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598
              |||||||| || ||||||||||||||||||||||||||||||||:||||:|||||||
Db        539 SLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDA 598

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||
Db        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 2
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             92.8%;  Score 3387;  DB 13;  Length 751;
  Best Local Similarity   86.9%;  Pred. No. 2.1e-195;
  Matches  654;  Conservative   18;  Mismatches   21;  Indels   60;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||||  |||||||||||||||||||||:||||||||||||:|||||||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||| |||  ||| |:|||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||| |||||||||||||||||||:|||||| ||||||||||||||||||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              |||||||||||||||:||||||:|||||||||||| ||||||:|||||    |:||:  ||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              :|:|||| ||:|||||: || || ||||||||||||||||||||||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG 298

Qy        289 ----------------------------------------------VPTTAASTPDAVDK 302
                                                           :||||||||||||
Db        299 PCRAMISRWYFDVAEGKCAPFFYGGCGGNRNNFDSEEYCMAVCGSVLPTTAASTPDAVDK 358

Qy        303 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 418

Qy        363 KVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKY 422
              |||||||||||||||||||||||||||||:|||||||||| ||||||||||||||||
Db        419 KVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKY 478

Qy        423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEE 482
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        479 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEE 538

Qy        483 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDD 542
              |||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        539 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEFSLDD 598

Qy        543 LQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602
              ||||| || |||||||||||||||||||||||||||||||:||||:||||||||||||
Db        599 LQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRH 658

Qy        603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        659 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 718

Qy        663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||
Db        719 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 3
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL       1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             88.0%;  Score 3214;  DB 13;  Length 693;
  Best Local Similarity   87.8%;  Pred. No. 4.8e-185;
  Matches  612;  Conservative   36;  Mismatches   43;  Indels    6;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| : ||:|    | ||||| ||| |||||||||||||:||||||||||||::| ||||
Db          1 MLPHITLLVLTV-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               || |||||||||||||||||||||||||||||||||:||||||:  | |:|||||||
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||:|||||||||||||:||||| :||:|||||||||||||
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFR 179
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVE 238
              |||||||| ||||:: ||||| ||||| |||||| || | |:|| ||    ||||| |||
Db        180 GVEFVCCPSAEESESFDSADA-EDDSDAWWGGADADYVDRSDDKAVEAQPDEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              ||| ||||| |||| ||| ||||||||||||||||||||||||||||||||| |||||||
Db        239 EEETDDDED--DGDEAEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRVPATAASTPD 296

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              ||||||| | ||||| | ||||||| ||||:||:||:|||||||||||||||||||||||
Db        297 AVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQ 356

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              ||||||||||||||||||||||||||||||||||||:|||||||||| |||||||||
Db        357 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNM 416

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
              |||||||||||||||||||||||||||||||||||||||||| |||||| |||| |||
Db        417 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA 476

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
              |||||||||||| |||||||||:::||:|: |:||||||||||:||||||||||:|||
Db        477 VAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEF 536

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598
              :::|||||||||| ||||||||||||||||||||||||||||||||||||||||||||:
Db        537 NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS 596

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
              |:|||: |||||||||||||:||||||||||||||||||||||||||||||||:|||
Db        597 EYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH 656

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||:||||||||||||||||||||
Db        657 GVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 693
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RESULT 4
Q98SF9
ID   Q98SF9      PRELIMINARY;      PRT;   695 AA.
AC   Q98SF9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein B.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
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DR   EMBL; AJ298151; CAC37194.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL       1     18       POTENTIAL.
SQ   SEQUENCE   695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

  Query Match             87.4%;  Score 3190;  DB 13;  Length 695;
  Best Local Similarity   87.2%;  Pred. No. 1.3e-183;
  Matches  609;  Conservative   39;  Mismatches   44;  Indels    6;  Gaps    5;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| : ||:| |  | ||||| ||| ||||||||||||:||||||||||||::| ||||
Db          1 MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               || ||||||||||||||||||||||||||||||||:||||||:  | |:|||||||
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||:|||||||||||||:||||  :||:||||||||||||||
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE 238
              |||||||| ||||:: ||||| |||||||||||| || | |:|| ||    ||||| |||
Db        180 GVEFVCCPTAEESESFDSADA-EDDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
              ||||||| |::|||| ||| |||||||||||||||||||||||||||| || || |||
Db        239 EEEADDD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRAVPATAVSTP 297

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              ||||||| | |||||  | ||||||| ||||:||:||:||||||||||||||||||||
Db        298 DAVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVI 357

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              |||||||||||||||||||||||||||||| ||||||:|||||||||| |||||||||
Db        358 QHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |||||||||||||||||||||||||||||||||||||||||||||| |||||| |||| ||
Db        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
              |||||||||||| |||||||||:::||:|: |:||||||||||:||||||||||:||
Db        478 AVAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGE 537

Qy        538 FSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMD 597
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                |:::|||||||||| |||||||||||||||||||||||||||||||||||| |||||||||
Db        538 FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD 597

Qy        598 AEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH 657
                :|:|||: ||||||||||||::|||||||||||||||||||||||||||||||||:|| 
Db        598 SEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657

Qy        658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
                |||||||||||||||||:||||||||||||||||||| 
Db        658 HGVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 695


RESULT 5
Q7ZXQ0
ID   Q7ZXQ0      PRELIMINARY;      PRT;   695 AA.
AC   Q7ZXQ0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC044324; AAH44324.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   695 AA;  78803 MW;  C1BD8AACC3356B05 CRC64;

  Query Match             87.3%;  Score 3188;  DB 13;  Length 695;
  Best Local Similarity   87.2%;  Pred. No. 1.8e-183;
  Matches  609;  Conservative   38;  Mismatches   45;  Indels    6;  Gaps    5;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| : ||:| |  | ||||| ||| |||||||||||||:||||||||||||::| ||||
Db          1 MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               || |||||||||||||||||||||||||||||||||:||||||:  | |:|||||||
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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                    ||||||||||||||||||||||:||||||||||||||:||||  :||:||||||||||||||
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE 238
              |||||||| ||||:: ||||| |||||||||||| || | |:|| ||    ||||| |||
Db        180 GVEFVCCPTAEESESFDSADA-EDDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
              ||||||| ||:|||| ||| ||||||||||||||||||||||||||||| || || |||
Db        239 EEEADDD-DDDDGDETEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRAVPATAVSTP 297

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              |||||||| | |||||  | ||||||| ||||:||:||:||||||||||||||||||||
Db        298 DAVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVI 357

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              |||||||||||||| |||||||||||||| ||||||:|||||||||| |||||||||
Db        358 QHFQEKVESLEQEAAKERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||| ||
Db        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
              |||||||||||| |||||||||:::||:|: |:||||||||||:||||||||||:||
Db        478 AVAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGE 537

Qy        538 FSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMD 597
              |:::|||||||| ||||||||||||||||||||||||||||||||||| |||||||||
Db        538 FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD 597

Qy        598 AEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH 657
              :|:|||: ||||||||||||::|||||||||||||||||||||||||||||||||:||
Db        598 SEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657

Qy        658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||:||||||||||||||||||
Db        658 HGVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 695
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RESULT 6
Q91963
ID   Q91963      PRELIMINARY;      PRT;   747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;
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RA   Okado H., Okamoto H.;
RT   "A Xenopus homologue of the human beta-amyloid precursor protein:
RT   developmental regulation of its gene expression.";
RL   Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR   EMBL; S52417; AAB24853.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   747 AA;  84893 MW;  A75E81885681D948 CRC64;

  Query Match             85.0%;  Score 3103;  DB 13;  Length 747;
  Best Local Similarity   81.0%;  Pred. No. 2.5e-178;
  Matches  598;  Conservative   35;  Mismatches   41;  Indels   64;  Gaps    5;

Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75
              ||||  ||| ||||||||||   |||||||||||||::| ||   || ||||||||||
Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
              |||||||||||||||||||||||:||||||:  | |:||||||||||||||||||||||
Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
              |||||||:|||||||||||||:||||| :||:||||||||||||||||||| ||||::
Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253
               ||||| ||| |||||||| || | |:|| ||    ||||| |||||| |||||  ||||
Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQPDEEEEVVEVEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------------------------- 288
               ||| ||||||||||||||||||||||||||||||
Db        250 AEEEPEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVTE 309

Qy        289 ------------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
                                           :| |||||||||||||| | ||||| |
Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377
              ||||||| ||||:||:||:|||||||||||||||||||||||||||||||||||| :|||
Db        370 KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429
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Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
              ||||||||||||||||||:||||||||||| |||||||||||||||||||||||||||||
Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
              |||||||||||||||||||||||| |||||| |||| |||||||||||||| ||||||
Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELFQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
              |||:::||:|: |:||||||||||:||||||||||:|||:::||||||||| ||||||
Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609

Qy        558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
              |||||||||||||||||||||||||||||||||||||:|:|||: ||||||||||||
Db        610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677
              |:||||||||||||||||||||||||||||||||||:||||||||||||||||||:||
Db        670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHHGVVEVDAAVTPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||
Db        730 QQNGYENPTYKFFEQMQN 747
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RESULT 7
O57394
ID   O57394      PRELIMINARY;      PRT;   699 AA.
AC   O57394;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   EL amyloid precursor protein 699.
GN   EL APP699.
OS   Narke japonica (Electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Narcinoidei; Narkidae; Narke.
OX   NCBI_TaxID=62965;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Electric lobe;
RX   MEDLINE=98129705; PubMed=9461486;
RA   Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA   Suzuki T.;
RT   "cDNA isolation of Alzheimer's amyloid precursor protein from
RT   cholinergic nerve terminals of the electric organ of the electric
RT   ray.";
RL   Biochem. J. 330:29-33(1998).
DR   EMBL; AB005544; BAA24230.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
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DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   699 AA;  78879 MW;  952915C309D50E5C CRC64;

  Query Match             81.2%;  Score 2964.5;  DB 13;  Length 699;
  Best Local Similarity   80.8%;  Pred. No. 4.9e-170;
  Matches  569;  Conservative   58;  Mismatches   58;  Indels   19;  Gaps    8;

Qy          2 LPG-LALLLLAAWTA-------RALEVPTDGNAGLL-AEPQIAMFCGRLNMHMNVQNGKW 52
              ||| | :|||||  |       |||||||| |||| ||||||||||:||||:||| |||
Db          5 LPGRLGMLLLAAAAALVLAPLCRALEVPTDGGAGLLAAEPQIAMFCGKLNMHVNVQTGKW 64

Qy         53 DSDPSGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFV 112
               ||||||  ||  ||||||:|||||||:||||||||||||:|||||||:||||||  ||| |
Db         65 VSDPSGTNTCFGTKEGILRYCQEVYPDLQITNVVEANQPITIQNWCKKGRKQCKGHPHIV 124

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              :|||||||||||||||||||||||:|:|| ||:||:|||||||||| :|  |||||||||
Db        125 VPYRCLVGEFVSDALLVPDKCKFLHREKMDTCESHLYWHTVAKETCGDKIMNLHDYGMLL 184

Qy        173 PCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEE 232
              |||||:||||||||||: ||:| :|| | :|:|||||||| | |||||  || |    ||
Db        185 PCGIDEFRGVEFVCCPIPEENDKIDS-DMDEEDSDVWWGGDDADYADGG-DKTV----EE 238

Qy        233 EVAEVEEEEADDDEDDEDGDEVEEE-AEEPYEEATERTTSIATTTTTTTESVEEVVRVPT 291
              :  | |||| : | |||| |::::|  |: ||: || |||   :|||||::||||||||
Db        239 KPIEEEEEEDESDIDDEDDDDLDDEVVEDQYEDPTEHTTS---STTTTTEAIEEVVRVPT 295

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              ||||||||||||||||||||:||||||||||||||||::||||||||||||||||||
Db        296 TAASTPDAVDKYLETPGDENEHAYFQKAKERLEAKHRERMSKIMREWEEAERQAKNLPKA 355

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ||||||| ||| |||||||||:||||||||||||||||||||:|||||: |||| |||
Db        356 DKKAVIQRFQEMVESLEQEAASERQQLVETHMARVEAMLNDRRRIALENYLAALQADPPR 415

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |||| | |||| ||||||||||||||:||| |||:|||||:||||||| || ||||||||
Db        416 PRHVLNALKKYSRAEQKDRQHTLKHFDHVRAVDPEKAAQIKSQVMTHLHVIDERMNQSLS 475

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| ||:|||||||||||||:|::| ||::|| :|: |||||||||:|||:|||||:||
Db        476 LLYKVPSVAEEIQDEVDELLQRERSYMDDMMANSVSDTRISYGNDALVPSLSETKTTIEL 535

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI 591
              || :||| |||||| | |  :|:|||||||||||||| |||||||||||| ||||||
Db        536 LPDDGEFILDDLQPPHPFVIESIPANTENEVEPVDARPAPDRGLTTRPGSGLTGIKTEEI 595

Qy        592 SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 651
              :|:||: ||: |||||||||||||| :|||||||||||||||||||||||||||||||||
Db        596 AELKMETEFQQDSGYEVHHQKLVFFPKDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 655

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||
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Db        656 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 699


RESULT 8
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             75.8%;  Score 2767.5;  DB 13;  Length 569;
  Best Local Similarity   93.5%;  Pred. No. 2.6e-158;
  Matches  535;  Conservative   14;  Mismatches   18;  Indels    5;  Gaps    4;

Qy        126 ALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFV 185
              ||||||||| |||||||||||||||||||:||||| ||||||||| ||||||||||||
Db          1 ALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLSCGIDKFRGVEFV 60

Qy        186 CCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVEEEEAD 243
              ||||||||||:||||||:|||||||||||| ||||||:|||||    |:||:  ||:|:||
Db         61 CCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVEDEDAD 120

Qy        244 DDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAVDKY 303
              || ||:|||||: || || |||||||||||||||||||||||||||||||||||||| ||||
Db        121 DD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDVVDKY 178

Qy        304 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 238
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Qy        364 VESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYV 423
              ||||||||||||||||||||||||||||||:|||||||||| ||||||||||||||||
Db        239 VESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKYV 298

Qy        424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI 483
              |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||
Db        299 RAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEEI 358

Qy        484 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDL 543
              ||||||||||||||||||||||||||||||||||:|||||||||||| ||||||||
Db        359 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPTLTETKTTVELLPVVGEFSLDDL 418

Qy        544 QPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603
              |||| || ||||||||||||||||||||||||||||||||:||||:||||||||||||
Db        419 QPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRHD 478

Qy        604 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEV 663
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        479 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVMLKKKQYTSIHHGVVEV 538

Qy        664 DAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||| |||||||||||||||||||||||||
Db        539 DAAVTP-ERHLSKMQQNGYENPTYKFFEQMQN 569
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RESULT 9
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
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DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             71.6%;  Score 2613;  DB 13;  Length 534;
  Best Local Similarity   94.8%;  Pred. No. 4.7e-149;
  Matches  506;  Conservative   13;  Mismatches   11;  Indels    4;  Gaps    3;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              ||||||||||||||||||||||||||||||:||||||:|||||||||||  ||||||:|
Db          3 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDD 62

Qy        224 KVVE--VAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTE 281
              ||||    |:||:  ||:|:|||| ||:||||: || || ||||||||||||||||||
Db         63 KVVEEQPEEDEELTVVEDEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTE 120

Qy        282 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 180

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        181 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENY 240

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ITALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 300

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IYERMNQSLSFLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 360

Qy        522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
              |||||||||||||:|||||||||||| || ||||||||||||||||||||||||||||||
Db        361 LTETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGS 420

Qy        582 GLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
              ||||:||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GLTNVKTEEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480

Qy        642 VITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 534


RESULT 10
Q7ZZT1
ID   Q7ZZT1      PRELIMINARY;      PRT;   678 AA.
AC   Q7ZZT1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid protein a variant 2.
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Investigation of zebrafish appa expression during embryogenesis.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY271746; AAP22958.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   678 AA;  76755 MW;  94163778444FD0BC CRC64;

  Query Match             70.3%;  Score 2567;  DB 13;  Length 678;
  Best Local Similarity   72.0%;  Pred. No. 3.7e-146;
  Matches  499;  Conservative   78;  Mismatches   94;  Indels   22;  Gaps   11;

Qy          5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCID 64
              | :||:|  :  |:|||:|   |||||||||||||:||||:|:|:|||: ||||:|:||
Db          6 LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSGSKSCIG 65

Qy         65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS 124
               |||||||||||||||||||||||||:| :|||: ||||::| | |:||||||||||
Db         66 NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS 125

Qy        125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
               ||||||||||||||||:||:||||||||||:| ::| |||||||||||||:||||||
Db        126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy        185 VCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD 244
               |||| |:     :||  ||||||||||||: || : |  :  : | |  |  :|::|  |
Db        186 VCCP-ADAGKESESAAVEEDDSDVWWGGAEADYTENSMTR--DAAAEPAV--LEDDEDAD 240

Qy        245 DEDDEDGD-EVEEEAEEPYEEATERTT-SIATTTTTTTESVEEVVRVPTTAASTPDAVDK 302
               :|:||||| : :|: ||  || |: |: :: :|||||||||||||||||| ::| |||||:
Db        241 EEEDEDGDGDRDEKIEEEEEERTQSTSAALTSTTTTTTESVEEVVRVPTPSSSPPDAVDR 300

Qy        303 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 362
               ||||| |||||||| |||| || ||||||||||||||||||||:||: ||||||||||
Db        301 YLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKSLPRNDKKAVIQHFQE 360

Qy        363 KVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKY 422
               |||:||||:|:||||||||||||||:||||||||||:|::|||| ||||||||::||||
Db        361 KVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQADPPRPRHVFSLLKKY 420

Qy        423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEE 482
               |||||||||||||||||||||||||||| ||:|||||| ||||||| ||| || ||::
Db        421 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVADD 480

Qy        483 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDD 542
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                |||:| ||||:||      |||: |: |:|||||||||  |     :||||
Db        481 IQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFGF 536

Qy        543 LQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602
                : |  ||       || |:||||||||  |  | ||| |||   | ::| |::|:|| ||
Db        537 IHP-ESFN----QPNTHNQVEPVDARPVPDLDLATRPVSGL---KPDDIPELRMEAEERH 588

Qy        603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 662
                  ||:||||||||||| |||||||||||||||||:||||||||:||||||||||::|
Db        589 S---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHHGIIE 645

Qy        663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
                |||||||||||||||||||||||||||||| |
Db        646 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 678


RESULT 11
Q90W28
ID   Q90W28      PRELIMINARY;      PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid precursor protein.
GN   APPA OR APP.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   738 AA;  83577 MW;  AF480F6D308FD298 CRC64;
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  Query Match             69.3%;  Score 2529;  DB 13;  Length 738;
  Best Local Similarity   66.4%;  Pred. No. 8e-144;
  Matches  501;  Conservative   79;  Mismatches   90;  Indels   84;  Gaps   14;

Qy          5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCID 64
              | :||:|  :  |:||||:|   |||||||||||||:||||:|:|:|||: ||||:|:||
Db          6 LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSGSKSCIG 65

Qy         65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS 124
               |||||||||||||||||||||||||:| :|||: ||||::| | |:||||||||||
Db         66 NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS 125

Qy        125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
              |||||||||||||||||:||:||||||||||:| ::| |||||||||||||:||||||
Db        126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy        185 VCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD 244
              |||| |:     :||  |||||||||||: || : |  :  : | |  | | ::|:||:
Db        186 VCCP-ADAGKESESAAVEEDDSDVWWGGAEADYTENSMTR--DAAAEPAVLE-DDEDADE 241

Qy        245 DED-DEDGD-----EVEEEAEEPYEEATERTT-SIATTTTTTTESVEEVVR--------- 288
              :|| |:|||     ::||| ||  || |: |: :: :|||||||||||||
Db        242 EEDEDQDGDGDRDEKIEEEEEE--EERTQSTSAALTSTTTTTTESVEEVVREVCFASAET 299

Qy        289 ------------------------------------------------VPTTAASTPDAVD 301
                                                             :|| ::| |||||
Db        300 GPCRAMLSRWYYVREERRCAPFIYGGCGGNRNNFESEEYCLSVCSGVLPTPSSSPPDAVD 359

Qy        302 KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQ 361
              :|||||  |||||||| |||| || |||||||||||||||||||:||: ||||||||||
Db        360 RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKSLPRNDKKAVIQHFQ 419

Qy        362 EKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKK 421
              ||||:||||:|:|||||||||||||:||||||||||:|::|||| ||||||||::|||
Db        420 EKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQADPPRPRHVFSLLKK 479

Qy        422 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAE 481
              |||||||||||||||||||||||||||||| ||:|||||| ||||||| ||| || ||:
Db        480 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD 539

Qy        482 EIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD 541
              :|||:| ||||:||      |||: |: |:|||||||||  |     :||||
Db        540 DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG 595

Qy        542 DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR 601
               : |  ||       || |:|||||||  |  | ||| |||   | ::| |::|:|| |
Db        596 FIHP-ESFN----QPNTHNQVEPVDARPVPDLDLATRPVSGL---KPDDIPELRMEAEER 647

Qy        602 HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVV 661
              |    ||:||||||||||| ||||||||||||||||:||||||||:||||||||||::
Db        648 HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHHGII 704

Qy        662 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||| |
Db        705 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 738
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RESULT 12
Q8UUR9
ID   Q8UUR9      PRELIMINARY;      PRT;   694 AA.
AC   Q8UUR9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative membrane protein.
GN   APPB.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315639; CAC85736.1; -.
DR   ZFIN; ZDB-GENE-020220-1; appb.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   694 AA;  79228 MW;  2B03382D411162DC CRC64;

  Query Match             68.1%;  Score 2487.5;  DB 13;  Length 694;
  Best Local Similarity   67.9%;  Pred. No. 2.3e-141;
  Matches  477;  Conservative   98;  Mismatches   97;  Indels   31;  Gaps    9;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
              |||:    : |:|||:| : |||||||:|||||:||||:|||:|||: ||:|||:|| ||
Db          9 LLLMLTTLSLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWEPDPTGTKSCISTK 68

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
              ||||:|||||||:|||||||||||||:|||||| ||:||::| | |:||||||||||||
Db         69 EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRRQCRSHTHIVVPYRCLVGEFVSDA 128

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
              ||||||||||||||||:||:||||||||||:| ::| |||||||||||||:||||||||
Db        129 LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC 188

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEVEE 239
              ||: |: | :|| : || :||||||||:|:| | |  :::|       | |::|    ||
Db        189 CPMEEQKD-LDSEEQEEANSDVWWGGAETEYTDASVLKEQVTAKPDPAVTEDDEDLNNEE 247
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Qy        240 EEADDDEDDEDGDEVEEEAEE-----PYEEATERTTSIA--TTTTTTTESVEEVVRVPTT 292
              ||  |:::| ||:: |:| ::       :: :|:|::||  |||||||||:||||||||
Db        248 EEVWDNDEDGDGEDDEDEEDDDEDIIDEQDTSEQTSNIAMTTTTTTTTESIEEVVRVPTM 307

Qy        293 AASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKAD 352
              | |  ||||:||| ||| |||  |||||| |||||||:||:||||||||||||||||:||
Db        308 APSPADAVDRYLEAPGDMNEHMRFQKAKESLEAKHREKMSEVMREWEEAERQAKNLPRAD 367

Qy        353 KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRP 412
              || :|| |||||||||:||| |||||||||||||||:|||||| |||:|:::||:  |||
Db        368 KKTIIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRRQALESYLSSLQSDQPRP 427

Qy        413 RHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSL 472
              | | |:||||:|||||||||||||||||| ||||||:|||  |||||||| |||||||
Db        428 RQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMTHLRVIEERMNQSLGY 487

Qy        473 LYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELL 532
              || || || :|||:|  |:|::|      |::: |: |:|||||||| | :: | :: |
Db        488 LYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDALMPDLPDSTTPLDNL 547

Qy        533 PVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEIS 592
              |   :  |  : |  ||      |||:| |||||||  :||| |||           ||
Db        548 PPEQD-GLGFIHP-ESFN----QANTDNHVEPVDARPIPERGLPTRP----------EIP 591

Qy        593 EVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQ 652
              :|::| | ||::||:|  ::|:| |||:|||||||||||||||||||||||||||:|||
Db        592 KVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQ 651

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||:|||||||||||||:||||||||||||||||||||
Db        652 YTSIHHGVIEVDAAVTPEERHLAKMQQNGYENPTYKFFEQMQN 694
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RESULT 13
Q9I9E7
ID   Q9I9E7      PRELIMINARY;      PRT;   612 AA.
AC   Q9I9E7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Slavov D.B., Gardiner K.;
RT   "An App cDNA from Zebrafish (Danio rerio).";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF257742; AAF71748.1; -.
DR   HSSP; P05067; 1HZ3.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
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DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   612 AA;  69710 MW;  59A9ACBDF9C59EFF CRC64;

  Query Match             64.1%;  Score 2339;  DB 13;  Length 612;
  Best Local Similarity   72.6%;  Pred. No. 1.7e-132;
  Matches  460;  Conservative   66;  Mismatches   80;  Indels   28;  Gaps   12;

Qy         68 GILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDAL 127
              |||||||||||||||||||||||||:| :|||: ||||::| | |:|||||||||||||
Db          1 GILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVSDAL 60

Qy        128 LVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCC 187
              |||||||||||||||:||:||||||||||:| ::| |||||||||||||:|||||||||
Db         61 LVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVCC 120

Qy        188 PLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDED 247
              | |:     :||  |||||||||||: || : |  :  : | |  |  :|::|  |:|:
Db        121 P-ADAGKESESAAVEEDDSDVWWGGAEADYTENSMTR--DAAAEPAV--LEDDEDADEEE 175

Qy        248 DEDGD-----EVEEEAEEPYEEATERTT-SIATTTTTTTESVEEVVRVPTTAASTPDAVD 301
              |||||     ::|||  ||  || |: |: :: :|||||||||:|||||||  ::| |||||
Db        176 DEDGDGDRDEKIEEEEEE--EERTQSTSAALTSTTTTTTESVDEVVRVPTPSSSPPDAVD 233

Qy        302 KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQ 361
              :|||||  |||||||| ||||  || |||||||||||||||||||:||: ||||||||||
Db        234 RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKSLPRNDKKAVIQHFQ 293

Qy        362 EKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKK 421
              ||||:||||:|:|||||||||||||:||||||||||:|::|||| ||||||||::|||
Db        294 EKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQADPPRPRHVFSLLKK 353

Qy        422 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAE 481
              |||||||||||||||||||||||||||||| ||:|||||| ||||||| ||| || ||:
Db        354 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD 413

Qy        482 EIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD 541
              :|||:| ||||:||      |||: |: |:|||||||||  |     :||||
Db        414 DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG 469

Qy        542 DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR 601
               : |  ||       || |:|||||||  |  | ||| |||   | ::| |::|:|| |
Db        470 FIHP-ESFN----QPNTHNQVEPVDARPVPDLDLATRPVSGL---KPDDIPELRMEAEER 521

Qy        602 HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVV 661
              |    ||:|||||||||| ||||||||||||||||:||||||||:||||||||::
Db        522 HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHHGII 578

Qy        662 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||| |
Db        579 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 612
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RESULT 14
Q8BPC7
ID   Q8BPC7      PRELIMINARY;      PRT;   384 AA.
AC   Q8BPC7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK076506; BAC36369.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   384 AA;  43990 MW;  A81B1AD8AE683173 CRC64;

  Query Match             52.8%;  Score 1928;  DB 11;  Length 384;
  Best Local Similarity   98.2%;  Pred. No. 4.7e-108;
  Matches  377;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        312 EHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEA 60

Qy        372 ANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQ 431
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         61 ANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLKKYVRAEQKDRQ 120

Qy        432 HTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELL 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELL 180

Qy        492 QKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGA 551
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        181 QKEQNHSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHPFGV 240

Qy        552 DSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQ 611
              |||||||||||||||||||||||||||||||||||||||||||||| ||||:|| ||
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Db        241 DSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFEVRHQ 300

Qy        612 KLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEE 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEE 360

Qy        672 RHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||
Db        361 RHLSKMQQNGYENPTYKFFEQMQN 384


RESULT 15
Q13861
ID   Q13861      PRELIMINARY;      PRT;   695 AA.
AC   Q13861;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Binding protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Vostrov A.A., Quitschke W.W., Schwarzman A.L., Blangy A., Cuzin F.,
RA   Wesley U.V., Hagag N.G., Goldgaber D.;
RT   "Cloning of a protein that binds to a recognition sequence in the APP
RT   promoter.";
RL   Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L19597; AAA35601.1; -.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
FT   NON_TER     695    695
SQ   SEQUENCE   695 AA;  79238 MW;  728CA8ACBB7594FB CRC64;

  Query Match             48.3%;  Score 1762;  DB 4;  Length 695;
  Best Local Similarity   50.8%;  Pred. No. 9.7e-98;
  Matches  366;  Conservative  113;  Mismatches  171;  Indels   70;  Gaps   17;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | ||||   || || :         |||    :||||||||||:||||:|:| |||: ||
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:| :||| :||||||:||||||||:|||| |:| |||:| :|||||   || |::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
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                ||||||||| ||||:||:| |:|||:||| | ||||| || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
                |:| | |:|||| :   :|   : |||:        : :  |  ||  |  :|    |:
Db        193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEDEEEDYDVYKSEFPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTTESVE 284
                :|:  | |  :||||:|:|:|| |: :        : | |  |  |   :  | : : :
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNE--ENPTEPGSDGTMSDKEIT 303

Qy        285 EVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQ 344
                  |:|| |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||||| |
Db        304 HDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQ 362

Qy        345 AKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITA 404
                |||||||::: :|||||  |::||:|||:|:|||||||:||||||||||||:|||||: |
Db        363 AKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAA 422

Qy        405 LQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
                ||: ||||  :   |::|||||  ||| ||::|::||  |||:||||::|||||| || |
Db        423 LQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEE 482

Qy        465 RMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTE 524
                | |||||||| || ||:|||:|:|||||:::       |:|          |    |::|
Db        483 RRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISE 525

Qy        525 TKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGL--------- 575
                |   |    |: | | ::: |:| |     ||  |||   |  :   | ||
Db        526 TPVDVR---VSSEES-EEIPPFHPF--HPFPALPENEGSGVGEQ---DGGLIGAEEKVIN 576

Qy        576 -TTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG 634
                   :    :   :| :: |:  :||     | |   : :    ||   :  |:|||:|
Db        577 SKNKVDENMVIDETLDVKEMIFNAE--RVGGLEEERESVGPLREDFSLSSSALIGLLVIA 634

Qy        635 VVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQ 694
                | |||||||:||||:|:|| :| ||:||||  :|||||||:||| :|||||||: ||||
Db        635 VAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENPTYKYLEQMQ 694
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Search completed: May 24, 2004, 15:14:05
Job time : 40.3333 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:02:24 ; Search time 10.3333 Seconds
(without alignments)
3512.216 Million cell updates/sec

Title: US-09-806-194A-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3590.5	98.3	770	1	A4_HUMAN	P05067 h amyloid b
2	3590.5	98.3	770	1	A4_MACFA	P53601 m amyloid b
3	3584	98.2	751	1	A4_SAISC	Q95241 s amyloid b
4	3535.5	96.8	770	1	A4_PIG	P79307 s amyloid b
5	3522.5	96.5	770	1	A4_CAVPO	Q60495 c amyloid b
6	3493.5	95.7	770	1	A4_MOUSE	P12023 m amyloid b
7	3493.5	95.7	770	1	A4_RAT	P08592 r amyloid b
8	2573	70.5	780	1	A4_TETFL	O73683 tetraodon f
9	2448.5	67.1	737	1	A4_FUGRU	O93279 fugu rubrip
10	1735	47.5	695	1	APP2_MOUSE	Q06335 mus musculu
11	1728	47.3	763	1	APP2_HUMAN	Q06481 homo sapien
12	1716	47.0	765	1	APP2_RAT	P15943 rattus norv
13	1190	32.6	650	1	APP1_HUMAN	P51693 homo sapien
14	1185	32.5	653	1	APP1_MOUSE	Q03157 mus musculu
15	817.5	22.4	686	1	A4_CAEEL	Q10651 caenorhabdi
16	748.5	20.5	887	1	A4_DROME	P14599 drosophila
17	292	8.0	59	1	A4_BOVIN	Q28053 bos taurus

18	288	7.9	58	1	A4_RABIT	Q28748 oryctolagus
19	288	7.9	58	1	A4_SHEEP	Q28757 ovis aries
20	287	7.9	58	1	A4_CANFA	Q28280 canis famil
21	283	7.8	57	1	A4_URSMA	Q29149 ursus marit
22	185.5	5.1	407	1	IE68_HSVSA	Q01042 herpesvirus
23	185.5	5.1	993	1	SCP1_MOUSE	Q62209 mus musculu
24	176	4.8	2004	1	MYS3_HUMAN	Q92794 homo sapien
25	175.5	4.8	802	1	NAB3_YEAST	P38996 saccharomyc
26	173.5	4.8	793	1	CALD_HUMAN	Q05682 homo sapien
27	172	4.7	771	1	CALD_CHICK	P12957 gallus gall
28	172	4.7	1498	1	GOA3_HUMAN	Q08378 homo sapien
29	169.5	4.6	297	1	TRT2_HUMAN	P45379 homo sapien
30	169.5	4.6	721	1	YCF2_OENPI	P31568 oenothera p
31	168.5	4.6	1875	1	MLP1_YEAST	Q02455 saccharomyc
32	168	4.6	1240	1	YNJ1_YEAST	P53935 saccharomyc
33	167.5	4.6	1976	1	MYHA_HUMAN	P35580 homo sapien
34	166.5	4.6	816	1	YG3A_YEAST	P53278 saccharomyc
35	166.5	4.6	1976	1	MYHA_RAT	Q9jlt0 rattus norv
36	164.5	4.5	1447	1	GOA3_MOUSE	P55937 mus musculu
37	163.5	4.5	681	1	MP10_HUMAN	O00566 homo sapien
38	163	4.5	2017	1	MYSN_DROME	Q99323 drosophila
39	162.5	4.5	712	1	NUCL_RAT	P13383 rattus norv
40	160.5	4.4	1976	1	MYHA_BOVIN	Q27991 bos taurus
41	160	4.4	694	1	NUCL_CHICK	P15771 gallus gall
42	159.5	4.4	1955	1	PUMA_PARUN	O61308 parascaris
43	158	4.3	301	1	TRT2_CHICK	P02642 gallus gall
44	157.5	4.3	706	1	NUCL_HUMAN	P19338 homo sapien
45	156.5	4.3	1332	1	SPT7_YEAST	P35177 saccharomyc

ALIGNMENTS

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RESULT 1
A4_HUMAN
ID   A4_HUMAN        STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).

RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.

RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [22]

Query Match 98.3%; Score 3590.5; DB 1; Length 770;
Best Local Similarity 90.1%; Pred. No. 9.8e-169;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 2
A4_MACFA
ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
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CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
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CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (POTENTIAL).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688    770       C83 (POTENTIAL).
FT   CHAIN       688    713       P3(42) (POTENTIAL).
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FT   CHAIN        688    711       P3(40) (POTENTIAL).
FT   CHAIN        712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN        714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN        721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN        740    770       C31 (POTENTIAL).
FT   DOMAIN        18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     700    723       POTENTIAL.
FT   DOMAIN       724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       732    751       INTERACTION WITH G(O)-ALPHA
FT                                  (BY SIMILARITY).
FT   DOMAIN       230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274    280       POLY-THR.
FT   SITE         144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                  (BY SIMILARITY).
FT   ACT_SITE     301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE         671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                  (BY SIMILARITY).
FT   SITE         706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                  (BY SIMILARITY).
FT   SITE         711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                  (BY SIMILARITY).
FT   SITE         713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                  (BY SIMILARITY).
FT   SITE         720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                  (BY SIMILARITY).
FT   SITE         724    734       BASOLATERAL SORTING SIGNAL
FT                                  (BY SIMILARITY).
FT   SITE         739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
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  Query Match             98.3%;  Score 3590.5;  DB 1;  Length 770;
  Best Local Similarity   90.1%;  Pred. No. 9.8e-169;
  Matches  694;  Conservative    1;  Mismatches    0;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLRKTTREPLTRD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 3
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
```

```
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
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DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        653    654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        685    685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
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FT   SITE        687    687       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        692    693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        694    695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        701    702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        705    715       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                (BY SIMILARITY).
FT   SITE        738    741       ENDOCYTOSIS SIGNAL.
FT   SITE        740    743       NPXY MOTIF.

  Query Match             98.2%;  Score 3584;  DB 1;  Length 751;
  Best Local Similarity   92.0%;  Pred. No. 2e-168;
  Matches  691;  Conservative    2;  Mismatches    2;  Indels    56;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||| ||||||||| |||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDHVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ----------------------------------------------VPTTAASTPDAVDKYL 304
                                                           :|||||||||||||||
Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVIPTTAASTPDAVDKYL 360

Qy        305 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 420

Qy        365 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 480

Qy        425 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 540

Qy        485 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        541 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 600

Qy        545 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 660

Qy        605 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 720

Qy        665 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||
Db        721 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751
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RESULT 4
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
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CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
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CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
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KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
```

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  Query Match             96.8%;  Score 3535.5;  DB 1;  Length 770;
  Best Local Similarity   88.4%;  Pred. No. 4.8e-166;
  Matches  681;  Conservative    8;  Mismatches    6;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||:||||||||||||||||||||||:|||||:||||||||||||:|||||||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||| ||||||| | |||||||||
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Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||:||||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              ||:||||||||||||||||||||||||||||||||||||||||||||
Db        241 EAEDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEHLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 5
A4_CAVPO
ID   A4_CAVPO   STANDARD;   PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid

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DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
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CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
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CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
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DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).

  Query Match             96.5%;  Score 3522.5;  DB 1;  Length 770;
  Best Local Similarity   88.2%;  Pred. No. 2.1e-165;
  Matches  679;  Conservative    7;  Mismatches    9;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||  |||||||||||||||||||||||||:|||||||||||: ||||||
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWEPDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| :|||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||:||||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              ||||||| ||||||||||||||||||:||||||||||||||||||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATEKTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RSMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQNLLKTSGEPVSQG 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
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Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 6
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
```

RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN=SAMP8; TISSUE=Hippocampus;
RX MEDLINE=21130647; PubMed=11235921;
RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA Alvarez J., Morley J.E.;
RT "Molecular cloning, expression, and regulation of hippocampal amyloid
RT precursor protein of senescence accelerated mouse (SAMP8).";
RL Biochem. Cell Biol. 79:57-67(2001).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN [6]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).

RN [8]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX MEDLINE=93287808; PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).
RN [11]
RP INTERACTION WITH KNS2.
RX MEDLINE=21010507; PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-I.";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22028091; PubMed=11912189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).
RN [14]
RP INTERACTION OF CTF PEPTIDES WITH NUMB.
RX MEDLINE=22008109; PubMed=12011466;
RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT "The gamma-secretase-generated intracellular domain of beta-amyloid

RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN [15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX MEDLINE=21437805; PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RT nuclear fraction of neurones in culture.";
RL J. Neurochem. 78:1168-1178(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions. Can promote transcription activation through binding
CC to APBB1/Tip60 and inhibit Notch signaling through interaction
CC with Numb. Couples to apoptosis-inducing pathways such as those
CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC similarity). Acts as a kinesin I membrane receptor, mediating the
CC axonal transport of beta-secretase and presenilin 1. May be
CC involved in copper homeostasis/oxidative stress through copper ion
CC reduction. Can regulate neurite outgrowth through binding to
CC components of the extracellular matrix such as heparin and
CC collagen I and IV (By similarity). The splice isoforms that
CC contain the BPTI domain possess protease inhibitor activity (By
CC similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.7%; Score 3493.5; DB 1; Length 770;
Best Local Similarity 87.8%; Pred. No. 5.5e-164;
Matches 676; Conservative 6; Mismatches 13; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| ||||||||||||||||||||||||:||||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||||||||||||| | ||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:|||||||||||||||||||||| ||||||||||||||:||||
Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||| |||||||||||||||||||||| ||||||||||||||||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGSVSTQSLLKTTSEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
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Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 7
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.

AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX MEDLINE=21443797; PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96187032; PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX MEDLINE=95263526; PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.

RX MEDLINE=97150061; PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX MEDLINE=99127916; PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX MEDLINE=99162676; PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX MEDLINE=99316162; PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [12]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX MEDLINE=21956095; PubMed=11959460;
RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochim. Biophys. Acta 1586:190-198(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=97239592; PubMed=9085254;

```
RA   Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA   Greengard P., Suzuki T.;
RT   "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT   phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT   cultured cells.";
RL   Mol. Med. 3:111-123(1997).
RN   [14]
RP   PHOSPHORYLATION ON SER-730.
RX   MEDLINE=99262094; PubMed=10329382;
RA   Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA   Greengard P., Nairn A.C., Suzuki T.;
RT   "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT   precursor protein at Ser655 by a novel protein kinase.";
RL   Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN   [15]
RP   PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP   THR-743.
RX   MEDLINE=99274744; PubMed=10341243;
RA   Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA   Kirino Y., Greengard P., Suzuki T.;
RT   "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT   during neuronal differentiation.";
RL   J. Neurosci. 19:4421-4427(1999).
RN   [16]
RP   PHOSPHORYLATION ON THR-743.
RX   MEDLINE=20396183; PubMed=10936190;
RA   Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA   Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT   "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT   protein by cyclin-dependent kinase 5.";
RL   J. Neurochem. 75:1085-1091(2000).
RN   [17]
RP   CARBOHYDRATE STRUCTURE OF APPICAN.
RX   MEDLINE=21463085; PubMed=11479316;
RA   Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA   Sugahara K., Robakis N.K.;
RT   "Appican, the proteoglycan form of the amyloid precursor protein,
RT   contains chondroitin sulfate E in the repeating disaccharide region
RT   and 4-O-sulfated galactose in the linkage region.";
RL   J. Biol. Chem. 276:37155-37160(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC       G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC       mediating the axonal transport of beta-secretase and presenilin 1
CC       (By similarity). May be involved in copper homeostasis/oxidative
CC       stress through copper ion reduction. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I and IV (By similarity). The
CC       splice isoforms that contain the BPTI domain possess protease
CC       inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
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CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity). Interacts,
CC       through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC       CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC       associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the

  Query Match             95.7%;  Score 3493.5;  DB 1;  Length 770;
  Best Local Similarity   87.7%;  Pred. No. 5.5e-164;
  Matches  675;  Conservative    8;  Mismatches   12;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| |||||||||||||||||||||||:||||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||::|||||||||||||||||||| |||||||||||||:||||
Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
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Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVSSQSLLKTTSEPLPQD 360
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Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
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Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||||||||| ||||:|| ||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 8
A4_TETFL
ID   A4_TETFL       STANDARD;      PRT;   780 AA.
AC   O73683;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
```

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CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                 HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE94520191D CRC64;

  Query Match             70.5%;  Score 2573;  DB 1;  Length 780;
  Best Local Similarity   65.4%;  Pred. No. 6e-119;
  Matches  513;  Conservative   71;  Mismatches   94;  Indels  106;  Gaps   10;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
              |||:|| :  | ||||| : |||||||:|||||::|||:|||:|||: ||||||:|| ||
Db          8 LLLVAAASTLAAEVPTDVSMGLLAEPQVAMFCGKINMHINVQSGKWEPDPSGTKSCIGTK 67

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
              ||||||||||||||||||||||||:||||||:||||||::| | |:|||||||||||||
Db         68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHMHIVVPYRCLVGEFVSDA 127

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEEFVC 186
              |||||||||||||||: ||:||||||||||:| ::: |||||||||||||:||||||||
```

```
Db        128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFVC 187

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS--------------EDKVVEVAEEE 232
              || ||   ::|| : : |||||||||||| ||:| |                  |||  ||
Db        188 CP-AEAERDMDSTEKDADDSDVWWGGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEEG 246

Qy        233 EVAEVEEEE------------------ADDDEDDEDGDEVEEEAEEPYEEATERTTSIA 273
              |||: ::||                  |||:|::|| ||::   |    :| | ||::|
Db        247 EVAQEDDEEEEEVLDTDQDGDGEEDHEAADDEEEEEDVDEIDAFGESDDVDADEPTTNVA 306

Qy        274 ---TTTTTTTESVEEVVR------------------------------------------ 288
                 ||||||||||||||
Db        307 MTTTTTTTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMN 366

Qy        289 ---------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQ 333
                           |||   |:||||| ||||| |||||||||||| ||||||||||
Db        367 NFESEEYCLSVCSSVVPTDMPSSPDAVDHYLETPADENEHAHFQKAKESLEAKHRERMSQ 426

Qy        334 VMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR 393
              |||||||||||||||:|||| ||| ||||||:|||||||:||||||||||||||:||||
Db        427 VMREWEEAERQAKNLPRADKKIVIQRFQEKVEALEQEAASERQQLVETHMARVEALLNDR 486

Qy        394 RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRS 453
              ||||||||:|||| ||||||||::|||||||||||||||||||||||||||||||||||
Db        487 RRLALENYLTALQQDPPRPRHVFSLLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRP 546

Qy        454 QVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              ||:|||||| ||||||| ||| || ||::|||:| ||||:||      |||: :: |:||
Db        547 QVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQREQAEMAQQLANLQTDVRVSY 605

Qy        514 GNDALMPSLTETKTTVELLPVNGEFSLDDLQPWH--SFGADSVPANTENEVEPVDARPAA 571
              |||||||          :|||   | :|  :   |  ||       ||||:||||||:||
Db        606 GNDALMPDQELGDGQADLLP--QEDTLGGVGFVHPESFN----QLNTENQVEPVDSRPTF 659

Qy        572 DRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLM 631
              :||: |||   :|    | : |::|: | |  : |||||||||||||||||||||||||
Db        660 ERGVPTRP---VTGKSMEAVPELRMETEDRQSTEYEVHHQKLVFFAEDVGSNKGAIIGLM 716

Qy        632 VGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
              |||||||||||||||||:|||||||||::|||||||||||||||||||||||||||||||
Db        717 VGGVVIATVIVITLVMLRKKQYTSIHHGIIEVDAAVTPEERHLSKMQQNGYENPTYKFFE 776

Qy        692 QMQN 695
              ||||
Db        777 QMQN 780
```

```
RESULT 9
A4_FUGRU
ID   A4_FUGRU       STANDARD;      PRT;   737 AA.
AC   O93279;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
```

```
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    737       ALZHEIMER'S DISEASE AMYLOID A4
FT                                 PROTEIN HOMOLOG.
FT   CHAIN       639    681       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    668       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    669    689       POTENTIAL.
FT   DOMAIN      690    737       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      286    344       BPTI/KUNITZ INHIBITOR.
FT   SITE        726    729       CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE    300    301       REACTIVE BOND.
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FT   DISULFID    290    340       BY SIMILARITY.
FT   DISULFID    299    323       BY SIMILARITY.
FT   DISULFID    315    336       BY SIMILARITY.
FT   CARBOHYD    522    522       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   737 AA;  82856 MW;  6FAD01E2E3B2B7E2 CRC64;
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  Query Match             67.1%;  Score 2448.5;  DB 1;  Length 737;
  Best Local Similarity   64.0%;  Pred. No. 6.9e-113;
  Matches  482;  Conservative   84;  Mismatches  100;  Indels   87;  Gaps   12;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
              :||| |   |: |:| |   ||| |||:|||||:||||:|||||||:||||||:|::||
Db          8 VLLLVATLTRSSEIPADDTVGLLTEPQVAMFCGKLNMHINVQNGKWESDPSGTKSCLNTK 67

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
              |||||||||||||||||||||||||:||||||:|||||::| | |:||||||||||||
Db         68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHTHIVVPYRCLVGEFVSDA 127

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
              |||||||||||||||: ||:||||||||||:| ::| |||||||||||||:||||:|||
Db        128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVKFVC 187

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS---EDKVVEVAEEEEVAEVEEEEAD 243
              || ||     ||:: | ::|||||||||| :|:: |     :   || :   |   :| |
Db        188 CP-AETEQETDSSEVEGEESDVWWGGADPEYSENSPPTPSRATYVAGD---AFERDENGD 243

Qy        244 DDEDDEDGDEVEEEAEEPYEEATERTTSIA--TTTTTTTESVEEVVR------------- 288
               |||:|| ::|:   |   :|: ||| ::|  ||||||||||||||
Db        244 GDEDEEDDEDVDPTDE---QESDERTANVAMTTTTTTTTESVEEVVRAVCWAQAESGPCR 300

Qy        289 ----------------------------------------VPTTAASTPDAVDKYLE 305
                                                     :|| | | |||||:| |
Db        301 AMLERWYFNPKKRRCVPFLFGGCGGNRNNFESEEYCLAVCSSSLPTVAPSPPDAVDQYFE 360

Qy        306 TPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVE 365
               |||:|||| |:|||| |||||||||||||||||||||||:|||||||||||||||
Db        361 APGDDNEHADFRKAKESLEAKHRERMSQVMREWEEAERQAKNLPRADKKAVIQHFQEKVE 420

Qy        366 SLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRA 425
              :|||||| |||||||||||||:|| |||| |||| |||| ||| | | ::|||||||
Db        421 ALEQEAAGERQQLVETHMARVEALLNSRRRLTLENYLGALQANPPRARQVLSLLKKYVRA 480

Qy        426 EQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQD 485
              |||||||||||:|||| |||||||||| ||:|||||| |||||||:||| ||:|| |||:
Db        481 EQKDRQHTLKHYEHVRTVDPKKAAQIRPQVLTHLRVIDERMNQSLALLYKVPSVASEIQN 540

Qy        486 EVDELLQKEQNYSDDVLANMIS---EPRISYGNDALMPSLTETKTTVELLPVNGEFSLDD 542
              ::      :     | : : :    :  :|||||||||    :   :: : |:|  |:|
Db        541 QIYPAAGSD---CKDPVEHCVCPQVDGLVSYGNDALMPDQAYSSAPMD-MGVDGLGSID- 595

Qy        543 LQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602
                  ||      ||||| |||||||| |||| |||   ::::| ||: ||: : : |
Db        596 ----QSFN----QANTENHVEPVDARPIPDRGLPTRP---VSSLKLEEMPEVRTETDKRQ 644

Qy        603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 662
               :||||:|||||||:|||||||||||||||||||||||||||:||||||||||:|
Db        645 SAGYEVYHQKLVFFADDVGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQYTSIHHGVIE 704
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Qy          663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
                ||||||||||||::||||||||||||||||||||
Db          705 VDAAVTPEERHLARMQQNGYENPTYKFFEQMQN 737


RESULT 10
APP2_MOUSE
ID   APP2_MOUSE     STANDARD;      PRT;   695 AA.
AC   Q06335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
GN   APLP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RA   von der Kammer H.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-246 FROM N.A.
RX   MEDLINE=94032480; PubMed=8218408;
RA   Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
RT   "The complete cDNA coding sequence for the mouse CDEI binding
RT   protein.";
RL   Biochim. Biophys. Acta 1216:154-156(1993).
RN   [3]
RP   SEQUENCE OF 185-695 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RX   MEDLINE=93129193; PubMed=1482349;
RA   Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT   "A murine sequence-specific DNA binding protein shows extensive local
RT   similarities to the amyloid precursor protein.";
RL   Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN   [4]
RP   SEQUENCE OF 1-35 FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96029629; PubMed=7592716;
RA   von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT   "The mouse APLP2 gene. Chromosomal localization and promoter
RT   characterization.";
RL   J. Biol. Chem. 270:25475-25480(1995).
CC   -!- FUNCTION: Binds to the DNA 5'-GTCACATG-3'(CDEI box) which plays
CC       an important role in the early development of embryos.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
CC       (Potential).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z22592; CAA80306.1; -.
DR   EMBL; M97216; AAA20039.1; -.
DR   EMBL; U34291; AAC52318.1; -.
DR   PIR; JC1404; JC1404.
DR   PIR; S38344; S38344.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88047; Aplp2.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Transmembrane; DNA-binding; Signal; Nuclear protein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    695       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    624       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    625    648       POTENTIAL.
FT   DOMAIN      649    695       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    294       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      218    231       POLY-GLU.
FT   DOMAIN      256    266       POLY-GLU.
FT   CARBOHYD    485    485       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    185    189       GMLLP -> MACCC (IN REF. 3).
SQ   SEQUENCE   695 AA;  78944 MW;  BBF4B95AAB2A0311 CRC64;

  Query Match             47.5%;  Score 1735;  DB 1;  Length 695;
  Best Local Similarity   49.3%;  Pred. No. 5.2e-78;
  Matches  360;  Conservative  118;  Mismatches  162;  Indels   90;  Gaps   19;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   || |  :         |||    :||||||| ||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
             :|||:|: ||| :|||||||:|||||||||:|||||| | :||:| ::|||:  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
             ||||||||| ||||| |:| |||||:||| |  |||: || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231
             |:| | |:|||| :  :||:  | : ||::          |  |  ||  :: :|   |
Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTTES 282
              :: :  |  || ::|||:|:|:|| |: :        : | |  |  |  ::  | : :
Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE 301

Qy        283 VEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 342
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                :   |:|| |   | | || |||| |:|||| ||||||:|| :|| || :| :||||||
Db        302 IVHDVKVPPTPLPTND-VDVYLETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAE 360

Qy        343 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYI 402
               ||||||| ::: :||||| |::||:|||:|:|||||||:||||||||||||:|||||:
Db        361 LQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYL 420

Qy        403 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 462
               |||: |||| :   |::|||| ||| ||::|::||  |||:||||::|||||| ||
Db        421 AALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVI 480

Qy        463 YERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSL 522
               || ||||:||| || ||:|||:|:|||||::: |:|  |  |:
Db        481 EERRNQSLTLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSI 523

Qy        523 TETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSG 582
               :|   | :   | :   | | |   |: :|||          |:  : | |
Db        524 SENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQDG-G 566

Qy        583 LTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NK 624
               |  : : | |: |||   |  :|  ::::| || ||                   :
Db        567 LIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFSLSS 624

Qy        625 GAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYEN 684
               |:|||:|  | |||||||:||||:|:|| :| ||:|||| :|||||||:||| :||||
Db        625 NALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYEN 684

Qy        685 PTYKFFEQMQ 694
               |||||: ||||
Db        685 PTYKYLEQMQ 694
```

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RESULT 11
APP2_HUMAN
ID   APP2_HUMAN     STANDARD;      PRT;   763 AA.
AC   Q06481;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE   (CDEI-box binding protein) (CDEBP).
GN   APLP2 OR APPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=93250009; PubMed=8485127;
RA   Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA   Norris K., Foster D.C.;
RT   "Molecular cloning of the cDNA for a human amyloid precursor protein
RT   homolog: evidence for a multigene family.";
RL   Biochemistry 32:4481-4486(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
```

RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT "A human amyloid precursor-like protein is highly homologous to a
RT mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA Hyman B.T., Neve R.L., Tanzi R.E.;
RT "Isolation and characterization of APLP2 encoding a homologue of the
RT Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a role in the regulation of hemostasis. The
CC soluble form may have inhibitory properties towards coagulation
CC factors. May interact with cellular G-protein signaling pathways.
CC May bind to the DNA 5'-GTCACATG-3'(CDEI box).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
CC (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q06481-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q06481-2; Sequence=VSP_000018;
CC Name=3;
CC IsoId=Q06481-3; Sequence=VSP_000019;
CC -!- TISSUE SPECIFICITY: In placenta, brain, heart, lung, liver, kidney
CC and endothelial tissues.
CC -!- SIMILARITY: Belongs to the APP family.

```
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S60099; AAC60589.1; -.
DR   EMBL; L09209; AAA35526.1; -.
DR   EMBL; Z22572; CAA80295.1; -.
DR   EMBL; L27631; AAC41701.1; -.
DR   EMBL; BC000373; AAH00373.1; -.
DR   PIR; A49321; A49321.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:598; APLP2.
DR   MIM; 104776; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0003677; F:DNA binding; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Signal; Alternative splicing; DNA-binding;
KW   Nuclear protein; Serine protease inhibitor.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    763       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    692       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    693    716       POTENTIAL.
FT   DOMAIN      717    763       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      215    280       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      306    364       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      215    231       POLY-GLU.
FT   ACT_SITE    320    321       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    310    360       BY SIMILARITY.
FT   DISULFID    319    343       BY SIMILARITY.
FT   DISULFID    335    356       BY SIMILARITY.
FT   VARSPLIC    308    363       Missing (in isoform 2).
FT                                /FTId=VSP_000018.
FT   VARSPLIC    613    624       Missing (in isoform 3).
FT                                /FTId=VSP_000019.
FT   CONFLICT    543    543       S -> I (IN REF. 1).
SQ   SEQUENCE   763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;
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Query Match             47.3%;  Score 1728;  DB 1;  Length 763;
Best Local Similarity   47.1%;  Pred. No. 1.3e-77;
Matches  372;  Conservative  112;  Mismatches  165;  Indels  140;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | ||||   || || :         |||    :|||||||||||:||||:|:| |||: ||
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:| :||| :||||||:||||||||:|||| |:| |||:| :||||:   || |::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||| ||||:||:| |:|||:||| | ||||| || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||| :   :|   : |||:        : :  |  ||  |  :|    |:
Db        193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEDEEEDYDVYKSEFPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTTSIATTTTTTTES 282
              :|:  | |  :||||:|:|:|| |: :  |          |  ||  :    :    |
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV-----------------------------------------------------VRVP 290
              |: |                                                     :|
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 350
               |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||||| |||||||
Db        366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 410
              |::: :|||||  |::||:|||:|:|||||||:||||||||||||:|||||: |||: ||
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
              ||  :   |::|||||| ||| ||::|::||  |||:||||::|||||| || || ||||
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSL 544

Qy        471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVE 530
              |||| || ||:|||:|:|||||:::       |:|          |    |::||   |
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISETPVDVR 587

Qy        531 LLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN----- 585
                 |: | | ::: |:| |     ||  |||    | :|     :  : |||:
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL 635

Qy        586 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKG 625
              |  ||    |: |:|     |   :|  ::::| || ||                  :
Db        636 IGAEEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSS 693

Qy        626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENP 685
              |:|||:|  | |||||||:||||:|:|| :| ||:|||  :||||||:||| :|||||
Db        694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENP 753
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```
Qy          686 TYKFFEQMQ 694
                ||||: ||||
Db          754 TYKYLEQMQ 762


RESULT 12
APP2_RAT
ID   APP2_RAT       STANDARD;      PRT;   765 AA.
AC   P15943;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN   APLP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-627 FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain, and Heart;
RX   MEDLINE=94368849; PubMed=8086458;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT   protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT   difference to human and murine homologues.";
RL   Biochim. Biophys. Acta 1219:167-170(1994).
RN   [2]
RP   SEQUENCE OF 575-765 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=90207205; PubMed=1690887;
RA   Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT   "Characterization of cDNA encoding a human sperm membrane protein
RT   related to A4 amyloid protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P15943-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P15943-2; Sequence=VSP_000021;
CC       Name=C;
CC         IsoId=P15943-3; Sequence=VSP_000020;
CC       Name=D;
CC         IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
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DR   EMBL; X77934; CAA54906.1; -.
DR   EMBL; M31322; AAA42352.1; -.
DR   PIR; A35981; A35981.
DR   PIR; S42880; S42880.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Alternative splicing; Serine protease inhibitor;
KW   Signal; Glycoprotein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    765       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    695       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    696    718       POTENTIAL.
FT   DOMAIN      719    765       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    282       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      308    366       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE    322    323       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    312    362       BY SIMILARITY.
FT   DISULFID    321    345       BY SIMILARITY.
FT   DISULFID    337    358       BY SIMILARITY.
FT   DOMAIN      218    229       POLY-GLU.
FT   CARBOHYD    628    628       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   VARSPLIC    311    365       Missing (in isoform C and isoform D).
FT                                /FTId=VSP_000020.
FT   VARSPLIC    616    627       Missing (in isoform B and isoform D).
FT                                /FTId=VSP_000021.
FT   CONFLICT    575    577       DQF -> EFV (IN REF. 2).
SQ   SEQUENCE   765 AA;  86882 MW;  CF51FCCCE305A0CF CRC64;

  Query Match             47.0%;  Score 1716;  DB 1;  Length 765;
  Best Local Similarity   46.2%;  Pred. No. 4.9e-77;
  Matches  364;  Conservative  122;  Mismatches  166;  Indels  136;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   || |  :         |||    :||||||||||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :||||||:|||||||||:|||||| | :||:| :|||::  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| ||||: |:| |||||:||| |  |||| || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192
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Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 233
              |:| | |:|||| : :|||: | : ||:: :      : ||| | ||       |:
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTTSIATTTTTTTESVEEVV 287
               | :|:| :::|::|:|:|| |: : |:         |  |  ::  | : : :   |
Db        249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R-------------------------------------------------------VPT 291
              :                                                       :|
Db        309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 368

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||||| ||||||||
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ::: :|||||  |::||:|||:|:|||||||:||||||||||||:|||||: |||: |||
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |  :   |::|||||| ||| ||::|::||  |||:||||::|||||||| || || |||||
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| || ||:|||:|:||||||:::      |:|          |    |::|    |
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN-----I 586
              |: | | ::: |:| |     |: :|||    | :|     :  : |||:       |
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELYHPM--KKGSGMAEQDGGLI 638

Qy        587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKGA 626
              ||    |: |||     |   :|  ::::| || ||                   :  |
Db        639 GAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSA 696

Qy        627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPT 686
              :|||:|  | |||||||:||||:|:|| :| ||:|||   :|||||||:||| :||||||
Db        697 LIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPT 756

Qy        687 YKFFEQMQ 694
              ||: ||||
Db        757 YKYLEQMQ 764
```

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RESULT 13
APP1_HUMAN
ID   APP1_HUMAN     STANDARD;      PRT;   650 AA.
AC   P51693; O00113; Q96A92;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN   APLP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98088960; PubMed=9428684;
RA Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
RA Masters C.L., Beyreuther K., Weidemann A.;
RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RT expression in COS-7 cells and identification of soluble forms in the
RT cerebrospinal fluid.";
RL Eur. J. Biochem. 250:354-363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98180887; PubMed=9521588;
RA Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA Olsen A., Tryggvason K.;
RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT 19q13.1.";
RL Hum. Genet. 102:192-196(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=96115107; PubMed=7494461;
RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA Black I.B.;
RT "Selective localization of amyloid precursor-like protein 1 in the
RT cerebral cortex postsynaptic density.";
RL Brain Res. Mol. Brain Res. 32:36-44(1995).
RN [5]
RP HEPARIN AND ZINC BINDING.
RX MEDLINE=95014513; PubMed=7929392;
RA Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT "The amyloid beta-protein precursor and its mammalian homologues.
RT Evidence for a zinc-modulated heparin-binding superfamily.";
RL J. Biol. Chem. 269:26618-26621(1994).

```
RN   [6]
RP   INTERACTION WITH APBA2.
RX   MEDLINE=99107877; PubMed=9890987;
RA   Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA   Sakiyama S., Kirino Y., Suzuki T.;
RT   "Interaction of a neuron-specific protein containing PDZ domains with
RT   Alzheimer's amyloid precursor protein.";
RL   J. Biol. Chem. 274:2243-2254(1999).
RN   [7]
RP   EXTRACELLULAR COPPER-BINDING.
RX   MEDLINE=22130992; PubMed=12135352;
RA   Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,
RA   Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
RA   Bayer T.A., Multhaup G.;
RT   "Evidence for a copper-binding superfamily of the amyloid precursor
RT   protein.";
RL   Biochemistry 41:9310-9320(2000).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, ALID1, activates transcription
CC       activation through APBB1 (Fe65) binding (By similarity). Couples
CC       to JIP signal transduction through C-terminal binding. May
CC       interact with cellular G-protein signaling pathways. Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC       serine phosphorylation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC       localized to the postsynaptic density (PSD).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clathrin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N- and O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
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DR   EMBL; U48437; AAB96331.1; -.
DR   EMBL; AD000864; AAB50173.1; -.
DR   EMBL; BC012889; AAH12889.1; -.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:597; APLP1.
DR   MIM; 104775; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    650       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN       621    650       C30 (BY SIMILARITY).
FT   DOMAIN       39    580       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    581    603       POTENTIAL.
FT   DOMAIN      604    650       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      158    178       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      204    211       ZINC-BINDING.
FT   DOMAIN      310    342       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      410    441       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      442    459       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      640    643       CLATHRIN-BINDING (POTENTIAL).
FT   DOMAIN      241    247       POLY-GLU.
FT   DOMAIN      264    268       POLY-GLU.
FT   SITE        167    167       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                                SIMILARITY).
FT   SITE        604    615       BASOLATERAL SORTING SIGNAL (BY
FT                                SIMILARITY).
FT   SITE        620    621       CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE        638    641       ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT   SITE        640    643       NPXY MOTIF.
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    551    551       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     48     48       A -> P (IN REF. 1).
SQ   SEQUENCE   650 AA;  72176 MW;  B95F0F4D1C5CBAC7 CRC64;

  Query Match             32.6%;  Score 1190;  DB 1;  Length 650;
  Best Local Similarity   38.8%;  Pred. No. 2.2e-51;
  Matches  272;  Conservative  115;  Mismatches  230;  Indels   84;  Gaps   16;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :|| | ||| |     :|   : | |      |:|  |||| :| ::: |:|: ||  ::
Db         23 LLPLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRSR 82

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCLV 119
               |:   : :|:||:::|||||  | :| | : :: ||   |     |||  |:|:|||
Db         83 RCLRDPQRVLEYCRQMYPELQIARVEQATQAIPMERWCGGSRSGSCAHPHHQVVPFRCLP 142
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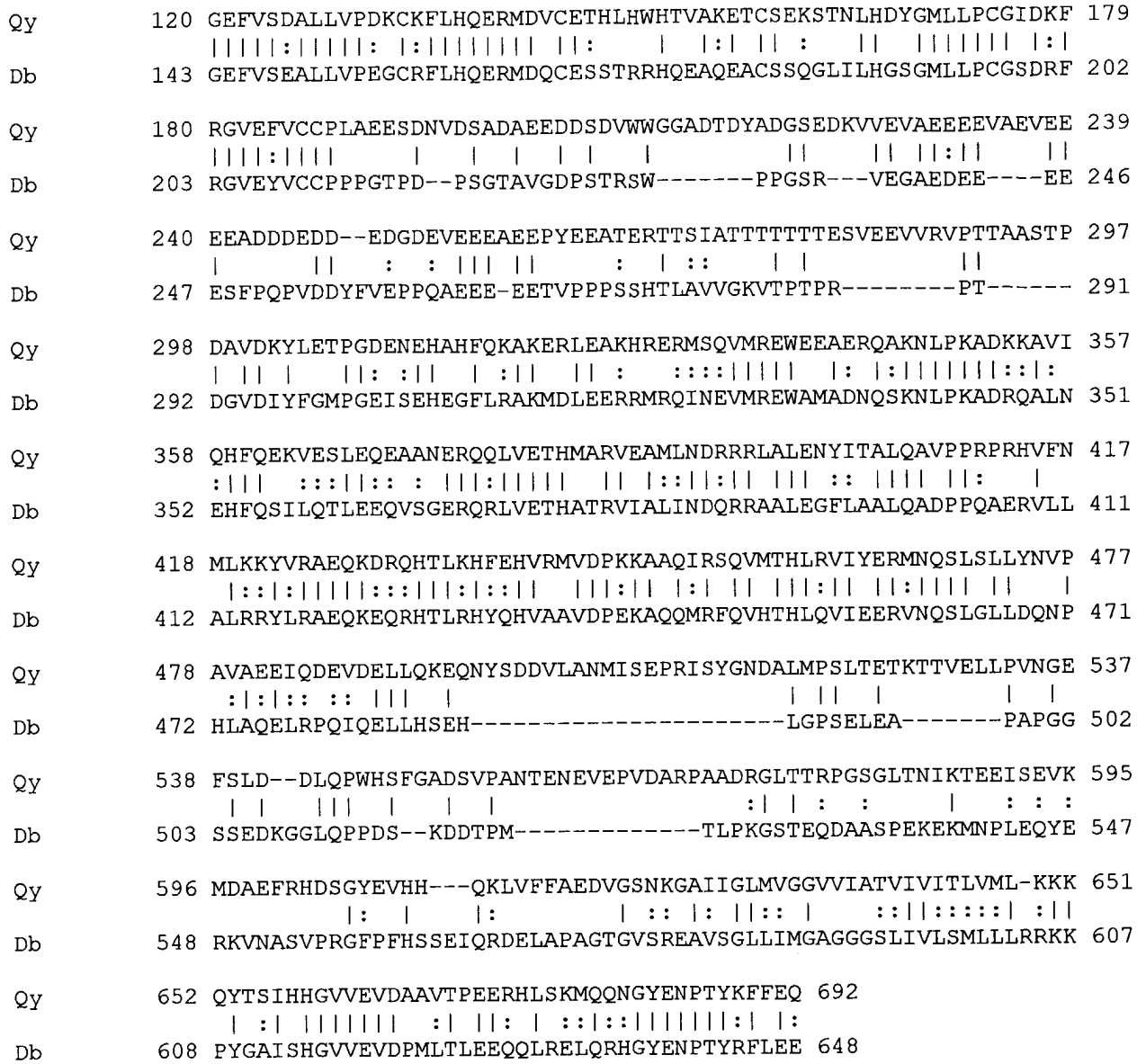

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Qy        120 GEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKF 179
Db        143 GEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDRF 202

Qy        180 RGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEE 239
Db        203 RGVEYVCCPPPGTPD--PSGTAVGDPSTRSW-------PPGSR---VEGAEDEE----EE 246

Qy        240 EEADDDEDD--EDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
Db        247 ESFPQPVDDYFVEPPQAEEE-EETVPPPSSHTLAVVGKVTPTPR--------PT------ 291

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
Db        292 DGVDIYFGMPGEISEHEGFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADRQALN 351

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
Db        352 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQADPPQAERVLL 411

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
Db        412 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVHTHLQVIEERVNQSLGLLDQNP 471

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
Db        472 HLAQELRPQIQELLHSEH----------------------LGPSELEA-------PAPGG 502

Qy        538 FSLD--DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVK 595
Db        503 SSEDKGGLQPPDS--KDDTPM-------------TLPKGSTEQDAASPEKEKMNPLEQYE 547

Qy        596 MDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKK 651
Db        548 RKVNASVPRGFPFHSSEIQRDELAPAGTGVSREAVSGLLIMGAGGGSLIVLSMLLLRRKK 607

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
Db        608 PYGAISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 648
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RESULT 14
APP1_MOUSE
ID   APP1_MOUSE     STANDARD;      PRT;   653 AA.
AC   Q03157; Q8VC38;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN   APLP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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RC TISSUE=Brain;
RX MEDLINE=93066322; PubMed=1279693;
RA Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP COLLAGEN-BINDING.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [4]
RP INTERACTION WITH DAB1.
RX MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT protein 1.";
RL J. Neurosci. 19:7507-7515(1999).
RN [5]
RP INTERACTION WITH MAPK8IP1.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP TYR-641.

```
RX   MEDLINE=22313598; PubMed=12228233;
RA   Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
RT   "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT   secretase regulates transcription.";
RL   J. Biol. Chem. 277:44195-44201(2002).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, ALID1, activates transcription
CC       activation through APBB1 (Fe65) binding. Couples to JIP signal
CC       transduction through C-terminal binding. May interact with
CC       cellular G-protein signaling pathways. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC       serine phosphorylation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clathrin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N- and O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L04538; AAA37247.1; -.
DR   EMBL; BC021877; AAH21877.1; -.
DR   PIR; A46362; A46362.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88046; Aplp1.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
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KW   Glycoprotein.
FT   SIGNAL        1     37       POTENTIAL.
FT   CHAIN        38    653       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN       624    653       C30 (BY SIMILARITY).
FT   DOMAIN       38    583       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    584    606       POTENTIAL.
FT   DOMAIN      607    653       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      157    177       COPPER-BINDING.
FT   DOMAIN      203    210       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      313    345       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      413    444       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      445    462       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      263    271       POLY-GLU.
FT   DOMAIN      535    538       POLY-SER.
FT   DOMAIN      601    606       POLY-LEU.
FT   SITE        166    166       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                                 SIMILARITY).
FT   SITE        607    618       BASOLATERAL SORTING SIGNAL (BY
FT                                 SIMILARITY).
FT   SITE        623    624       CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE        641    644       ENDOCYTOSIS SIGNAL.
FT   SITE        643    646       NPXY MOTIF.
FT   CARBOHYD    464    464       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    554    554       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN     641    641       Y->G: REDUCED BINDING OF APBB1.
FT   CONFLICT     17     17       P -> PP (IN REF. 2).
SQ   SEQUENCE   653 AA;  72750 MW;  56516DC3EA40E4B0 CRC64;

  Query Match             32.5%;  Score 1185;  DB 1;  Length 653;
  Best Local Similarity   38.6%;  Pred. No. 3.9e-51;
  Matches  270;  Conservative  121;  Mismatches  231;  Indels   78;  Gaps   17;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
              :|| |:|||| |  |   | | :   |      |:|  |||| :| ::: |:|: ||  :
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
              : |:   : :|:||:::|||| |  | :| | : :: ||   |     |||  |:|: ||
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
               |||||:|||||: |:|||||||| ||:    |  |:| || :   ||  ||||||| |:
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
               |||||:||||    : |     | :  :  |  ||     |:| ||       ||||
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
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Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
               | || |   ||:  ||  | :||  || :   ::::|||||  |: |:|||||||::|:
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
```

```
              :|||  :::||:: : |||:|||||  || |::||:|| ||| :: |||  ||:   |
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |::|:|||||:::|||:|::||  |||:|| |:| || |||:|| ||||||| ||   |
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
              :|:|:: :: |||          ||  :    :    || :| | :| |
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
                    |||             |:: :|    |   :| | :  |     |   : : :
Db        511 ----GSLQP------------PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551

Qy        597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKKQ 652
                       |:  |    |:        | :: |: ||:: |    ::||::|::| |||
Db        552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKP 611

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
              | :| |||||||  :| ||: | ::|::|||||||:| |:
Db        612 YGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651
```

```
RESULT 15
A4_CAEEL
ID   A4_CAEEL       STANDARD;      PRT;   686 AA.
AC   Q10651; Q18583; Q95ZX1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APL-1 OR C42D8.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE OF 6-686 FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=94089766; PubMed=8265668;
RA   Daigle I., Li C.;
RT   "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT   the human beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Hallsworth K.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   REVISIONS, AND ALTERNATIVE SPLICING.
RA   Waterston R.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
```

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CC       Name=a;
CC         IsoId=Q10651-1; Sequence=Displayed;
CC       Name=b;
CC         IsoId=Q10651-2; Sequence=VSP_000017;
CC         Note=No experimental confirmation available;
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U00240; AAC46470.1; ALT_INIT.
DR   EMBL; U56966; AAA98722.1; -.
DR   EMBL; U56966; AAK68242.1; -.
DR   PIR; T15795; T15795.
DR   HSSP; P05067; 1MWP.
DR   WormPep; C42D8.8a; CE04209.
DR   WormPep; C42D8.8b; CE27845.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW   Alternative splicing.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    686       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN       22    621       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    622    642       POTENTIAL.
FT   DOMAIN      643    686       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      205    228       ASP-RICH.
FT   DOMAIN      676    679       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD     84     84       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    538    539       Missing (in isoform b).
FT                                /FTId=VSP_000017.
SQ   SEQUENCE   686 AA;  79434 MW;  A0816858FDD48608 CRC64;

  Query Match             22.4%;  Score 817.5;  DB 1;  Length 686;
  Best Local Similarity   29.1%;  Pred. No. 3.9e-33;
  Matches  222;  Conservative  110;  Mismatches  275;  Indels  155;  Gaps   22;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :: || : :| | |  |   |          | :|  ||  | :|  : | | :|
Db          6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||   |  ||:||:: || : |||:|| :  |:| :||:     ||   | | || |: |
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122
```

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN------LHDYGMLLPC 174
              || |:|| ||  |:| |    | |  : ||   | : |  | :       :  : :| ||
Db        123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
               :| | ||||||||    :|  :  | ::
Db        183 ALDMFTGVEFVCCP----NDQTNKTDVQKTK---------------------------- 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
                 |:|: ||||||   |:  ||::|  ||
Db        210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE---------------------------- 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
               | : | | :     |||  |:||: |:: |||::: :||:|| :      |::||: |
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
              |  :|   |    ||: | |||:|    |:::   |  ||:||||:::| |  :|  ||
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
                   |    |   || |:|||:||| |||  : |:   | |:||  :  |:  || |
Db        355 THVNKPNKHSVLQSLKAYIRAEEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              |:| :|::| : |         ||   :: :|||   :  |    |  |  :| :   |
Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANT---ENEVEP 564
                 |   |: |    :     ::||     | ::   ::    |     |   : :|:
Db        471 NAKLDVKAPTTTAKPVKETDNAKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy        565 VDARP--------------------AADRGLTTRPGSGLTNIKTEE-----ISEVKMDA 598
              || :|                    |        |  |: :::|     | |:::|
Db        531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
              |         :|||        ||:   |   |        ::   :  | | |    :
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
               :      | :|||   ||||||:: || ||||||| ||:
Db        643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683
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Search completed: May 24, 2004, 15:12:01
Job time : 13.3333 secs